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(54) **DNAS AND PROTEINS OR PEPTIDES SPECIFIC TO BACTERIA OF THE SPECIES *NEISSERIA MENINGITIDIS*, PROCESSES FOR OBTAINING THEM AND THEIR BIOLOGICAL USES**

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(30) **Foreign Application Priority Data**

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(51) **Int. Cl.**
C12Q 1/68 (2006.01)

(52) **U.S. Cl.** **435/6**; 435/183; 435/252.3; 435/320.1; 435/69.3; 536/23.7; 536/24.32; 536/24.33; 514/44

(58) **Field of Classification Search** 435/6, 435/91.2, 252.3, 320.1, 183, 69.3; 514/44; 536/23.7, 24.32, 24.33, 23.1, 23.2, 23.3
See application file for complete search history.

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(57) **ABSTRACT**

The DNA of the invention are characterised in that they concern the whole or part of genes, with their reading frame, to be found in *Neisseria meningitidis*, but not in *Neisseria gonorrhoeae*, or in *Neisseria lactamica* except the genes involved in the biosynthesis of the polysaccharide capsule, frp A, frp C, opc, por A, rotamase the sequence IC1106, IgA protease, pilline, pilC, transferrin binding proteins and opacity proteins. The invention also concerns the polypeptides corresponding to these DNA and the antibodies directed against these polypeptides. It is applicable in the prevention and the detection of meningococcus induced infections and meningitis.

8 Claims, 9 Drawing Sheets

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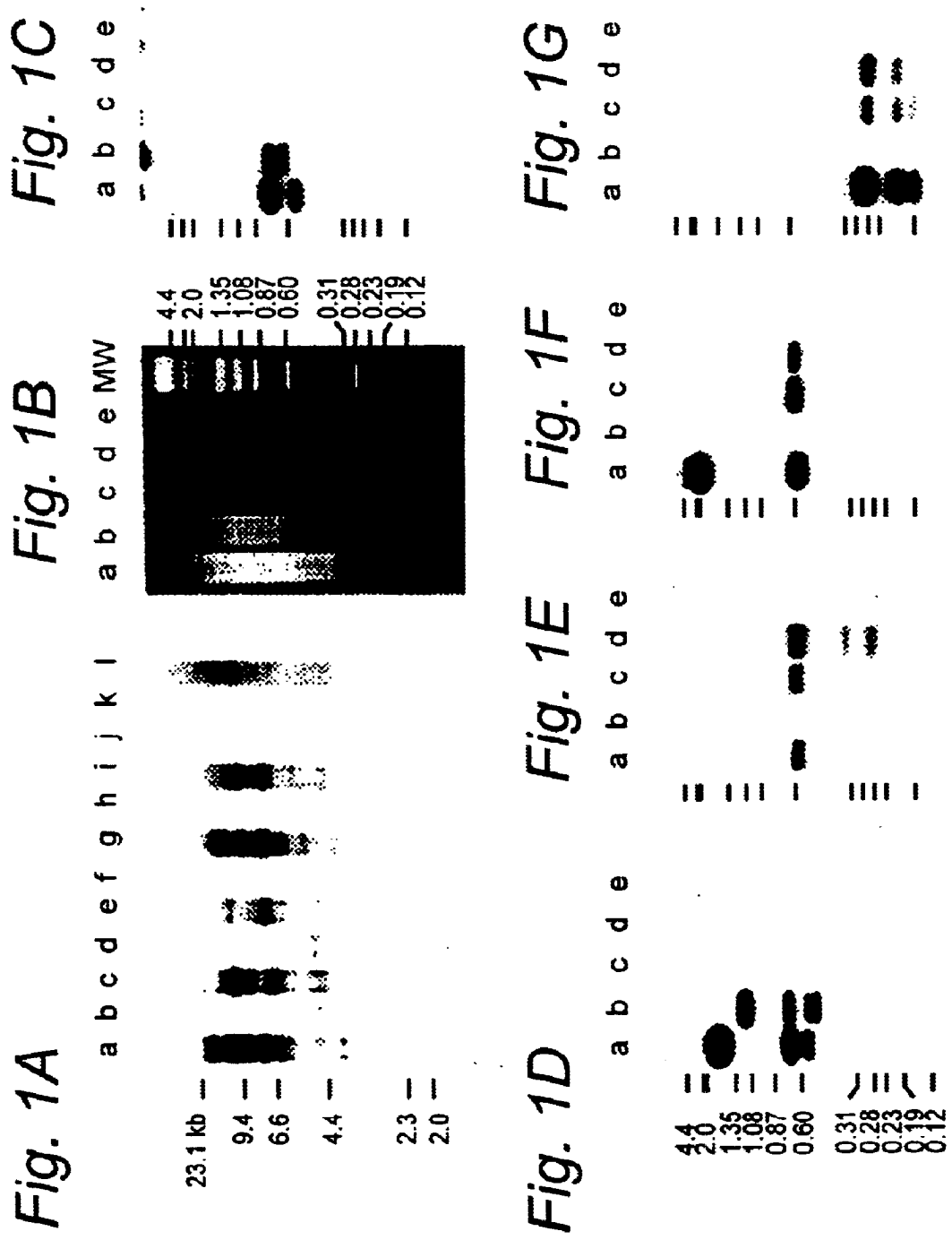
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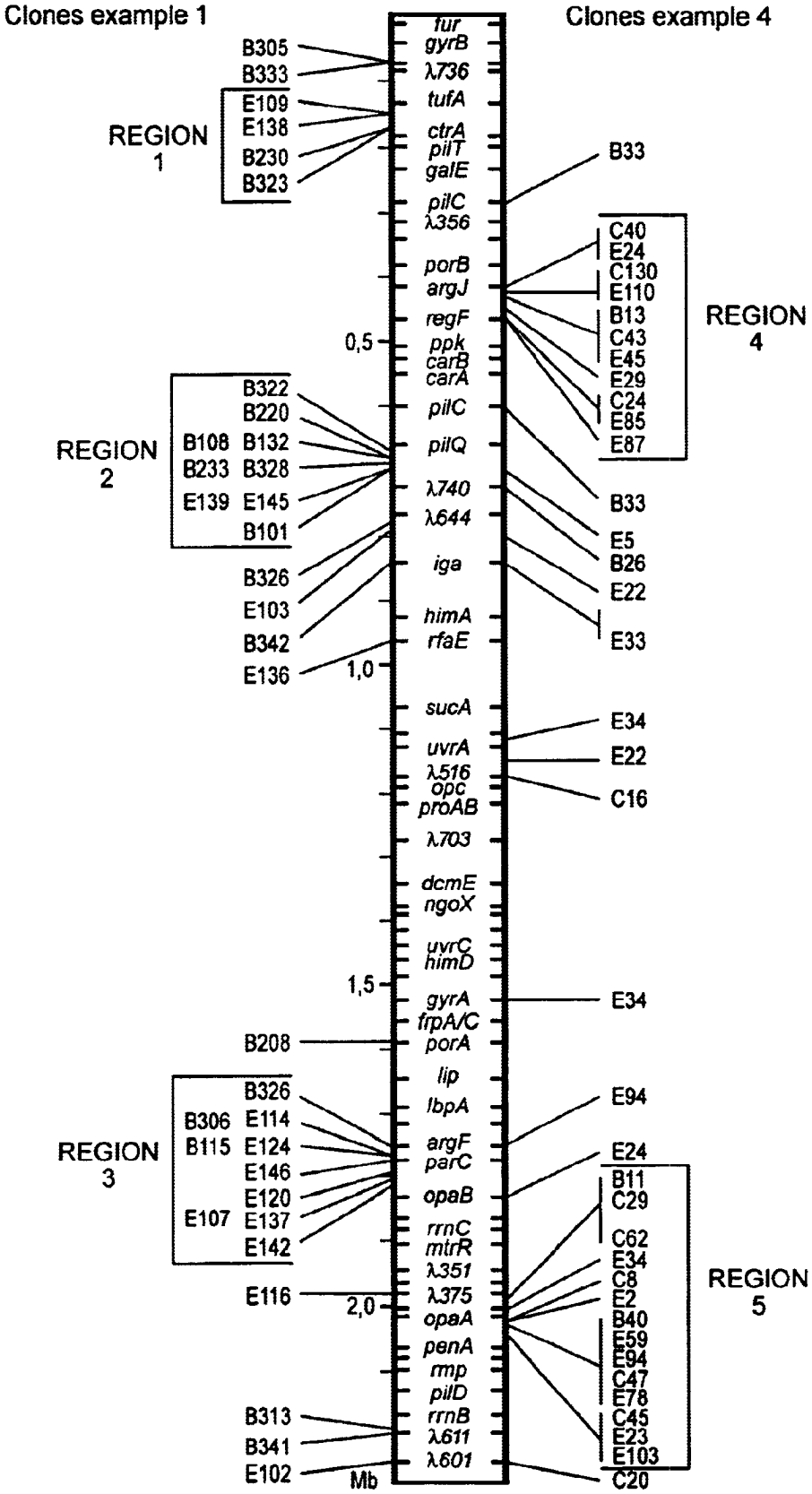
6.6
4.4
2.3
2.0
Fig. 1B
a b c d e MW
4.4
2.0
1.35
1.08
0.87
0.60
0.31
0.28
0.23
0.19
0.12
Fig. 1C
a b c d e
Fig. 1D
a b c d e
4.4
2.0
1.35
1.08
0.87
0.60
0.31
0.28
0.23
0.19
0.12
Fig. 1E
a b c d e
Fig. 1F
a b c d e
Fig. 1G
a b c d e

Fig. 2


Clones example 1
Clones example 4
REGION 1
REGION 2
REGION 3
REGION 4
REGION 5
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B333
E109
E138
B230
B323
B322
B220
B108
B132
B233
B328
E139
E145
B101
B326
E103
B342
E136
B208
B326
B306
E114
B115
E124
E146
E120
E107
E137
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B313
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E102
B33
C40
E24
C130
E110
B13
C43
E45
E29
C24
E85
E87
B33
E5
B26
E22
E33
E34
E22
C16
E34
E94
E24
B11
C29
C62
E34
C8
E2
B40
E59
E94
C47
E78
C45
E23
E103
C20
fur
gyrB
λ736
tufA
ctrA
pilT
galE
pilC
λ356
porB
argJ
regF
ppk
carB
carA
pilC
pilQ
λ740
λ644
iga
himA
rfaE
sucA
uvrA
λ516
opc
proAB
λ703
dcmE
ngoX
uvrC
himD
gyrA
frpA/C
porA
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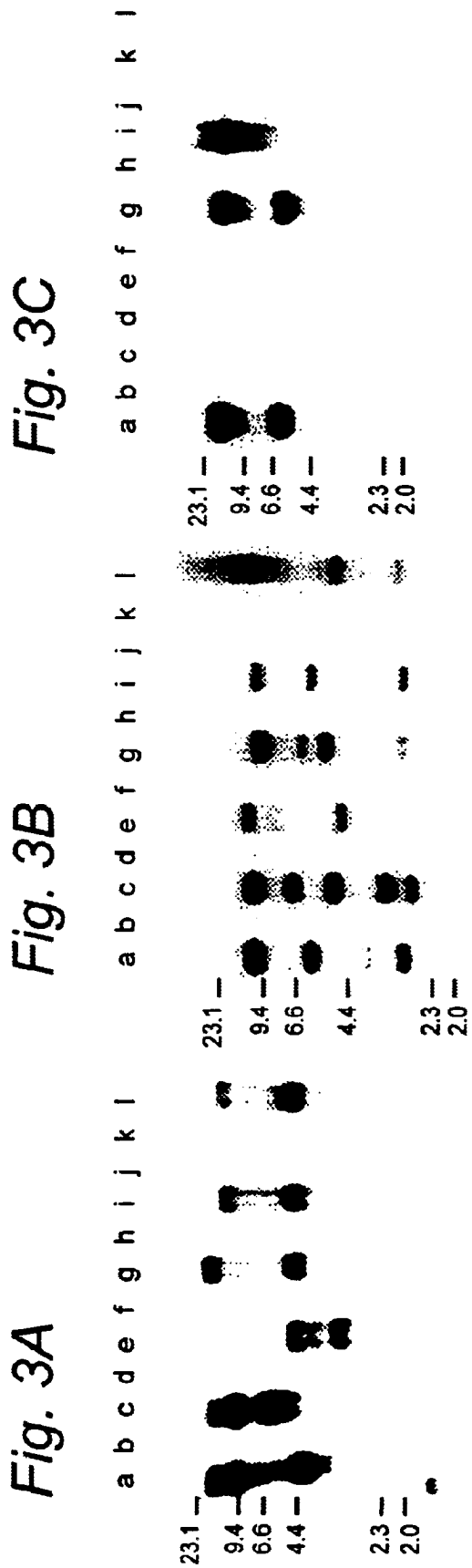
Fig. 3A
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9.4
6.6
4.4
2.3
2.0
Fig. 3B
a b c d e f g h i j k l
23.1
9.4
6.6
4.4
2.3
2.0
Fig. 3C
a b c d e f g h i j k l
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6.6
4.4
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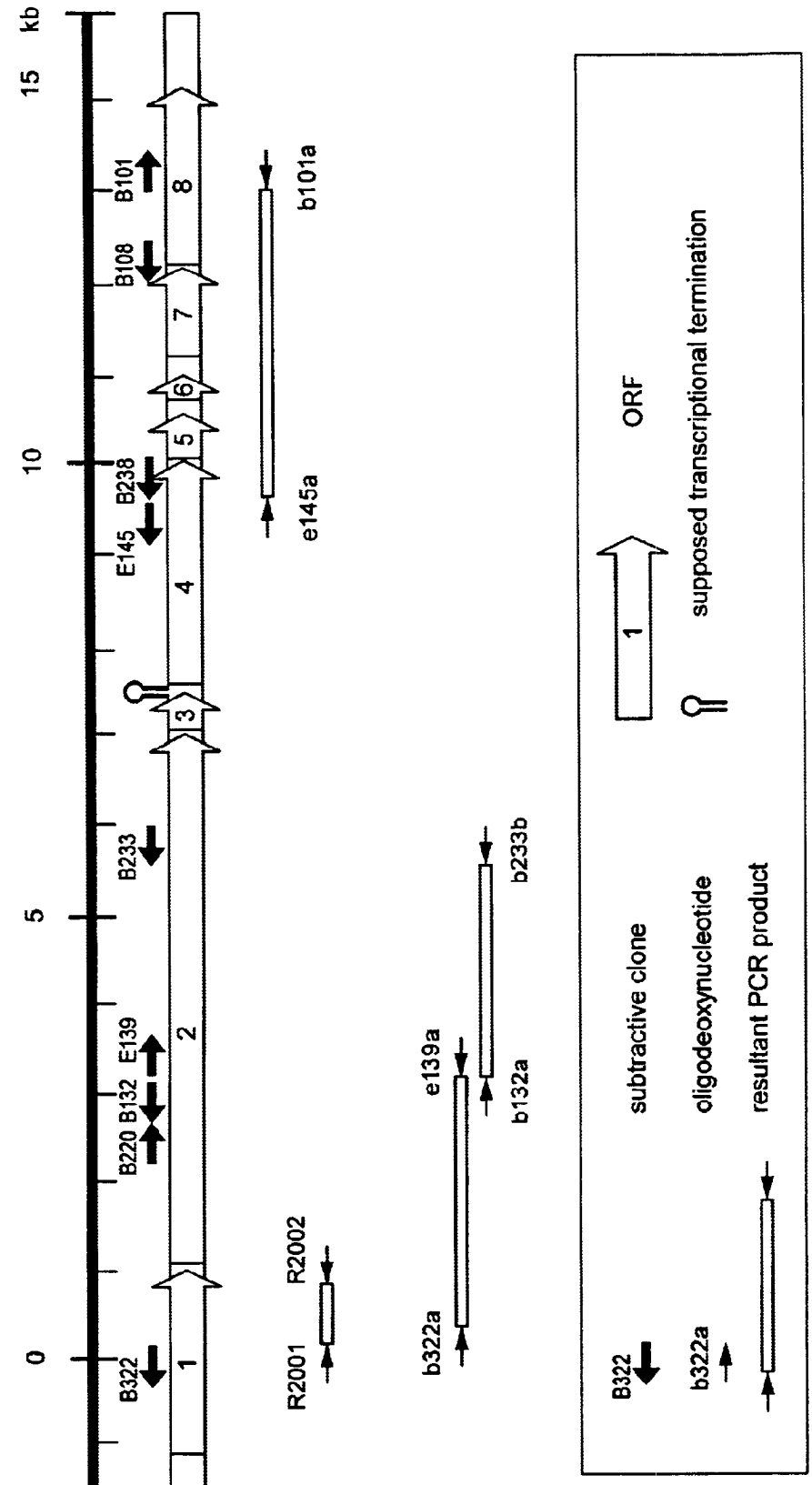
2.0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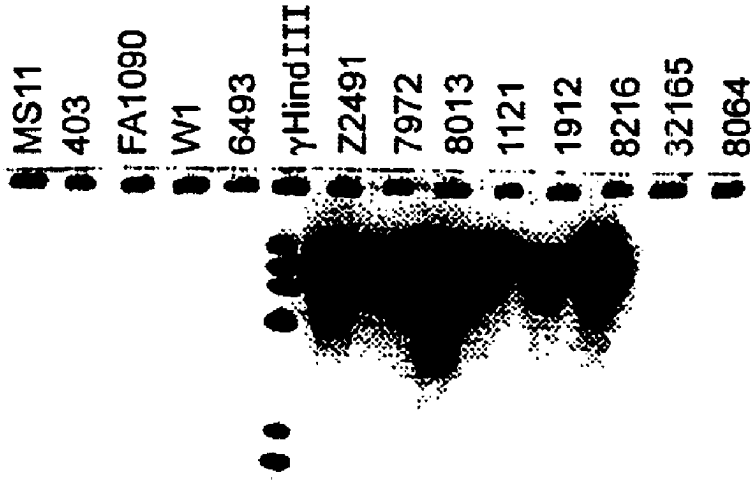
E139
B233
B238
E145
B108
B101
R2001
R2002
b322a
e139a
b132a
b233b
e145a
b101a
subtractive clone
oligodeoxynucleotide
resultant PCR product
ORF
supposed transcriptional termination

Fig. 4

Fig. 5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Z2491
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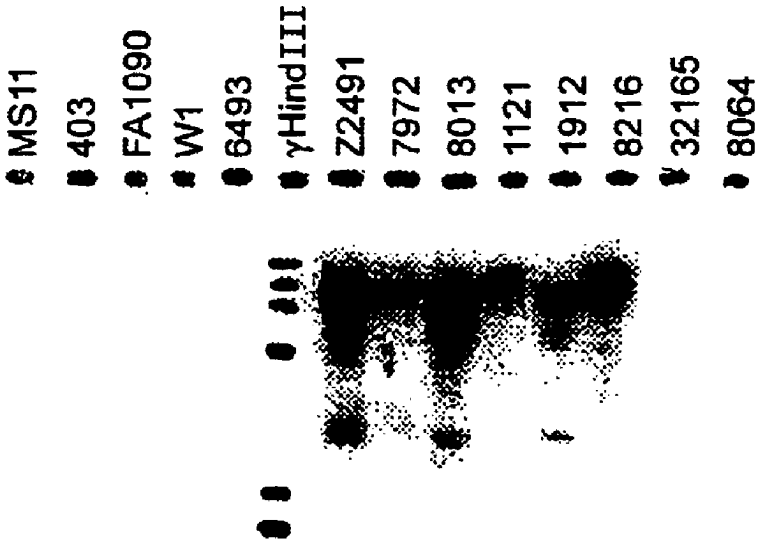
8013
1121
1912
8216
32165
8064

Fig. 6


MS11
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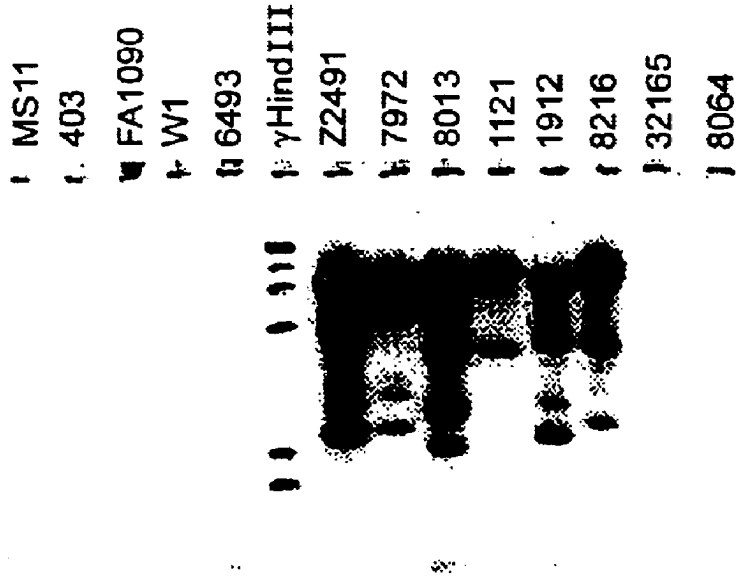
FA1090
W1
6493
γHindIII
Z2491
7972
8013
1121
1912
8216
32165
8064

Fig. 7


MS11
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FA1090
W1
6493
γHindIII
Z2491
7972
8013
1121
1912
8216
32165
8064

Fig. 8A

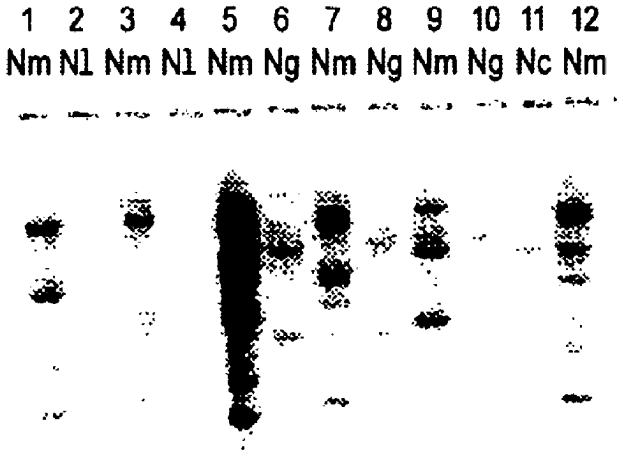
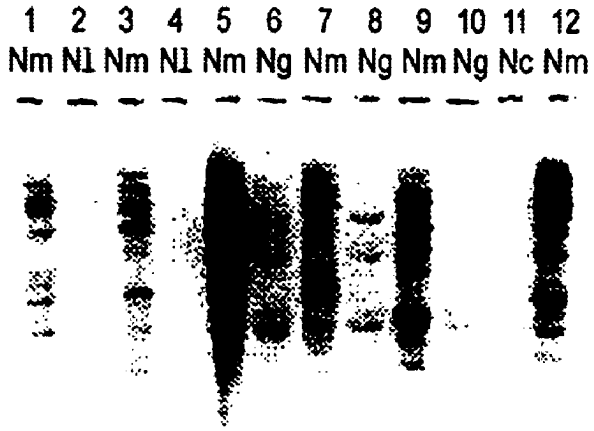

1 2 3 4 5 6 7 8 9 10 11 12
Nm Nl Nm Nl Nm Ng Nm Ng Nm Ng Nc Nm

Fig. 8B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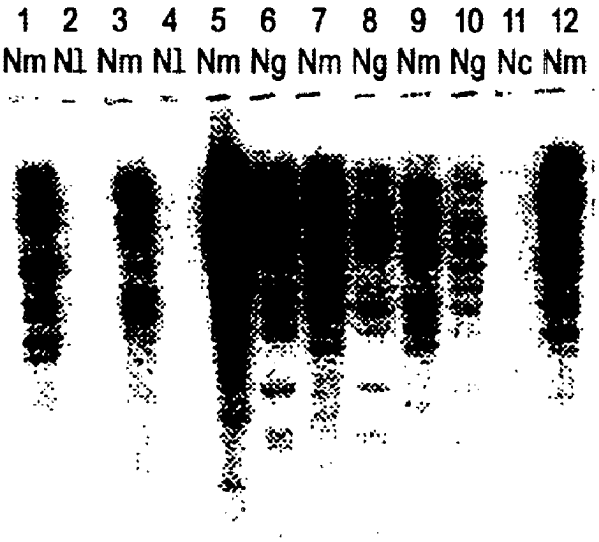
Nm Nl Nm Nl Nm Ng Nm Ng Nm Ng Nc Nm

Fig. 8C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Nm Nl Nm Nl Nm Ng Nm Ng Nm Ng Nc Nm

Fig. 9

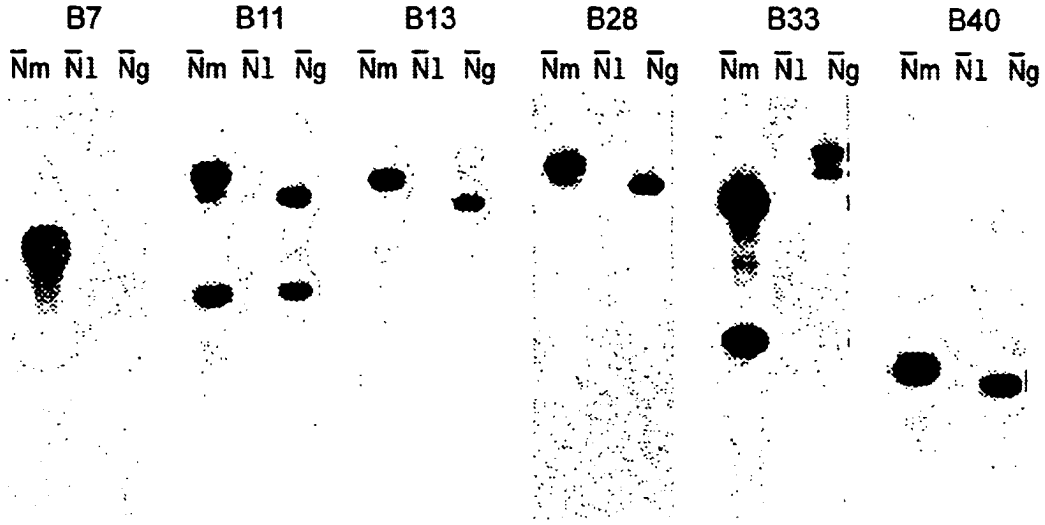
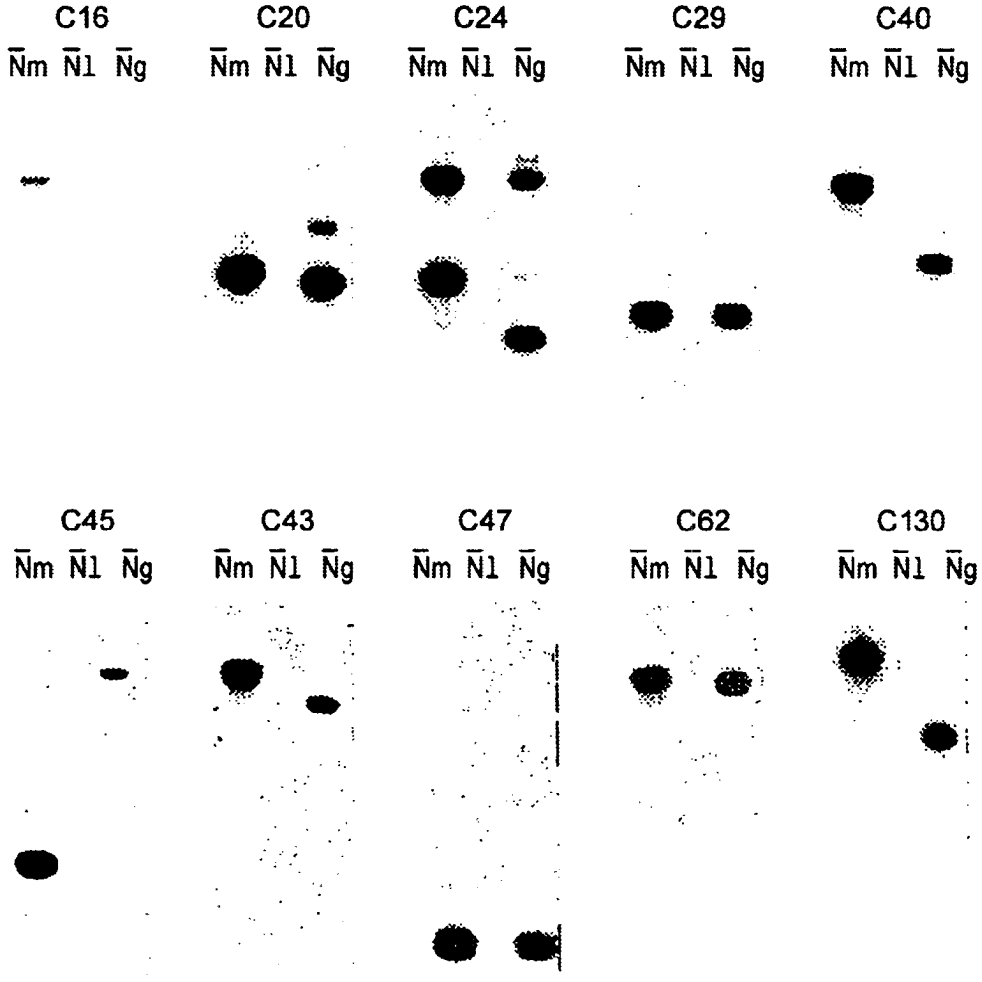

B7
B11
B13
B28
B33
B40
Nm N1 Ng

Fig. 10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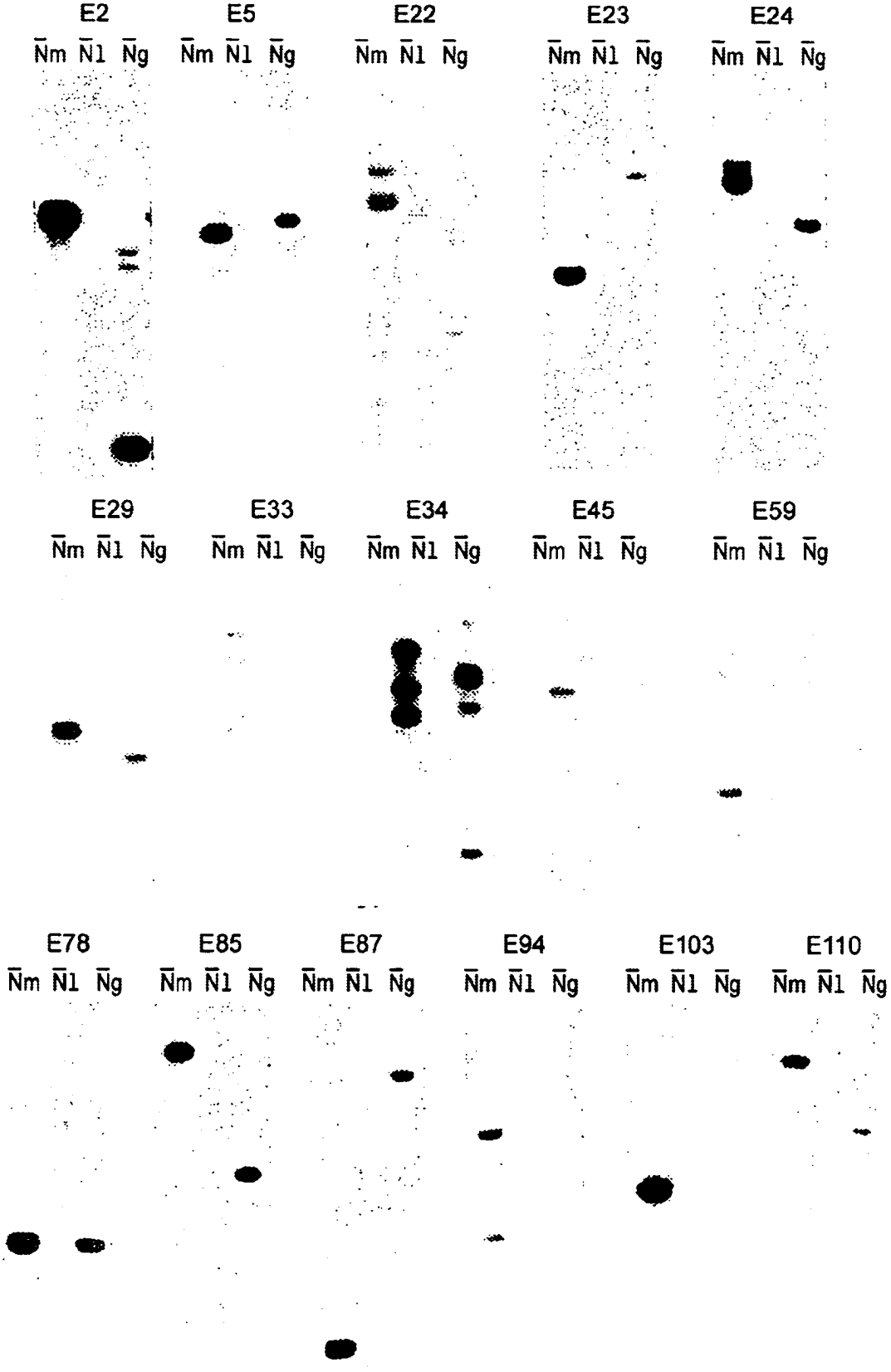
C20
C24
C29
C40
C45
C43
C47
C62
C130
Nm N1 Ng

Fig. 11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E5
Nm N1 Ng
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Nm N1 Ng
E94
Nm N1 Ng
E103
Nm N1 Ng
E110
Nm N1 Ng

DNAS AND PROTEINS OR PEPTIDES SPECIFIC TO BACTERIA OF THE SPECIES *NEISSERIA MENINGITIDIS*, PROCESSES FOR OBTAINING THEM AND THEIR BIOLOGICAL USES

The present application is a continuation of application Ser. No. 09/214,759, filed Apr. 22, 1999 now abandoned, which is a 371 application of PCT/FR97/01295, filed Jul. 11, 1997, and claims benefit of FR 96 08768, filed Jul. 12, 1996.

DNAs and proteins or peptides specific to bacteria of the species *Neisseria meningitidis*, processes for obtaining them and their biological uses.

The invention relates to DNAs and to proteins and peptides which are specific to bacteria of the species *Neisseria meningitidis* (abbreviated below to Nm), to the process for obtaining them and to their biological uses, in particular for the prevention and detection of meningococcal infections and meningitis.

It is known that Nm is one of the main agents of cerebrospinal meningitis.

Studies conducted in the United States have shown that 5 to 10% of the population are asymptomatic carriers of the Nm strain(s). The transmission factors of Nm are poorly known. For a proportion of persons infected, Nm penetrates the bloodstream, where it can cause meningococcaemia and/or progress to the cerebrospinal stream, to cause meningitis. Without fast antibiotic treatment, the infection can develop like lightning and become fatal.

Compared with other pathogens, Nm has the characteristic of being able to cross the haemato-encephalic barrier to colonize the meninges. The study of the pathogenicity of Nm is therefore important not only in the context of meningitis, but also in the context of any disease which affects the brain.

The benefit of having available tools specific to this species of bacteria for the uses envisaged above is therefore understood.

Genetically, Nm is very close to bacteria of the species *Neisseria gonorrhoeae* (abbreviated to Ng below) and of the species *Neisseria lactamica* (abbreviated to Nl below). However, their pathogenicity is very different.

Nm colonizes the nasopharynx, and then crosses the pharyngeal epithelium to invade the submucous space, thus being responsible for septicaemia and meningitis.

Ng is especially responsible for infections located in the genitourinary tract. It colonizes the genital mucosa, and then crosses the epithelium, subsequently invading the subepithelium, where it multiplies and is responsible for a severe inflammatory reaction. Disseminated gonococcal infections are possible, but remain rare and are the result of only some strains.

As regards Nl, it is considered that this is a non-pathogenic strain, since it is not responsible for a localized or general invasion.

A first consideration thus led to taking into account the fact that Nm and Ng, while being bacteria very close to one another, have different pathogenic potencies.

Since the genome of these bacteria has a high homology, only limited parts of the genome of Nm and Ng must code for specific virulence factors responsible for their pathogenesis.

It is clear that Nm has, compared with Ng, DNA sequences which are specific to it and which must be involved in the expression of its specific pathogenic potency.

The species Nm is subdivided into serogroups based on the nature of the capsular polysaccharides.

At least 13 serogroups have been defined, among which serogroups A, B and C are responsible for about 90% of meningitis cases. Groups A and C are found in epidemic forms of the disease. Group B is the serogroup generally isolated the most in Europe and the United States.

The capsule, which is present in Nm and absent from Ng, has served as the basis for formulating meningococcal antimeningitis vaccines.

The polysaccharides of the Nm capsule have been used to formulate a vaccine which has proved to be effective in preventing in adults the meningitis caused by meningococci of serogroups A, C, W135 and Y.

However, the polysaccharide of Nm group C has proved to be weakly immunogenic in children of less than two years, while the polysaccharide of Nm group B is non-immunogenic in man and shares epitopes with adhesion glycoproteins present in human neuronal cells.

There is therefore no universal vaccine capable of preventing infections caused by all the serogroups of the meningococci and capable of responding to the intrinsic antigenic variability of bacterial pathogens in general and Nm in particular.

Because of the cross-reactivity of the Nm group B polysaccharide with human antigens, the multiplicity of the serogroups and the antigenic variability of Nm, the strategies proposed to date cannot lead to a vaccine which is effective in all situations.

Research is therefore concentrated on study of the characteristic elements responsible for the specificity of the meningococcal pathogenesis.

The majority of genes which have been studied in either of the two bacteria Nm or Ng have their homologue in the second bacterium.

In the same way, the majority of virulence factors identified to date in Nm have a counterpart in Ng, that is to say pilin, the PilC proteins, the opacity proteins and the receptors of lactoferrin and transferrin.

The specific attributes of meningococci characterized in the prior art are the capsule, the Frp proteins analogous to RTX toxins, Opc proteins of the external member, glutathione peroxidase, the porin PorA and the rotamase gene.

Among these, only the capsule is invariably present in the virulent strains of Nm. However, several extracellular pathogens have a capsule without nevertheless crossing the haemato-encephalic barrier.

Attributes which have not yet been identified must therefore be responsible for the specificity of the meningococcal pathogenesis. These attributes are probably coded by DNA sequences present among the meningococci but absent from the gonococci.

The inventors have developed a new approach based on subtractive isolation of Nm-specific genes, which genes must be linked to the specific pathogenesis of Nm, and more particularly to crossing of the haemato-encephalic barrier.

The subtractive method developed in the prior art has resulted in the production of epidemological [sic] markers for some Nm isolates. These markers are of limited use: they do not cover all the serogroups of the Nm species.

In contrast to these studies, the work of the inventors has led, by confronting Nm with the entire Ng chromosome sheared in a random manner, to the development of a means for cloning all the DNAs present in Nm and absent from Ng, thus providing tools of high specificity with respect to Nm, and thus enabling the genetic variability of the species to be responded to for the first time.

The terms "present" and absent" used in the description and claims in relation to the DNAs of a strain or their

expression products are interpreted on the basis of identical hybridization conditions (16 h at 65° C., with $NaPO_4$ 0.5 M, pH 7.2; EDTA-Na 0.001 M, 1%, 1% bovine serum albumin and 7% sodium dodecylsulphate) using the same probe and the same labelling intensity of the probe, the same amount of chromosomal DNA and the same comparison element (chromosomal DNA of the homologous strain).

It is therefore considered that the DNA is present if the signal obtained with the probe is practically the same as that obtained with the reference strain.

Conversely, it is considered that the DNA is absent if this signal appears very weak.

A second consideration of the pathogenicities of Nm and Ng leads to taking into account their common capacity for colonization and penetration of the mucosa, and then invasion of the subepithelial space of the latter. It is highly probable that this process involves virulence factors common to the two pathogens. In this respect, it is known that a certain number of virulence factors have already been identified in Nm and in Ng, such as the pili proteins, PilC, the opacity proteins, the IgA proteases, the proteins for binding to transferrin and to lactoferrin, and the lipooligosaccharides.

The approach of the inventors is thus extended to investigation of the Nm regions which are specific to Nm and Ng but absent from the non-pathogenic species Nl, and in a general manner to investigation of the chromosomal regions of the DNAs and their expression products specific to a given species by the means developed in accordance with the invention.

The object of the invention is thus to provide DNAs of Nm specific to its pathogenic potency and means for obtaining them, in particular by formulating banks formed exclusively from these Nm-specific DNAs.

It also provides the products derived from these DNA sequences.

The invention also relates to the utilization of specific and exhaustive characteristics of these banks to formulate tools which can be used, in particular, in diagnostics, treatment and prevention.

The DNAs of the invention are characterized in that they are in all or part genes, with their reading frame, present in *Neisseria meningitidis*, but absent either from *Neisseria gonorrhoeae* and from *Neisseria lactamica*, with the exception genes involved in the biosynthesis of the polysaccharide capsule, frpA, frpC, opc, por A, rotamase, the sequence IS1106 (Accession No. Z 11857 in the EMBL/GenBank/DDBJ Nucleotide Sequence Data Libraries; see Knight et al., 1992, Molecular Microbiology 6(11): 1565–1573), IgA proteases, pilin, pilC, proteins which bind transferrin and opacity proteins.

As stated above, the terms "present" and "absent" are interpreted on the basis of the hybridization conditions used in the Southern blotting described in the examples and referred to above.

It can be seen that these DNAs include variants where these express a function intrinsic to the Nm species, more particularly a phenotype found solely in Nm or in common exclusively with Ng.

According to a main aspect, these DNAs are specific to the pathogenicity of *Neisseria meningitidis*, in spite of the genetic variability of this species.

According to an embodiment of the invention, the said DNAs are specific to Nm, in contrast to Ng.

More particularly, the Nm-specific DNAs are absent from *Neisseria lactamica* and from *Neisseria cinerea*.

Surprisingly, the majority of genetic differences between the strains of meningococci and those of gonococci appear grouped in distinct regions, which are said to correspond to the pathogenicity islets described previously for *E. coli* and *Y. pestis*.

In a preferred embodiment of the invention, these DNA are thus also characterized in that they comprise one or more sequence(s) present on the chromosome of *Neisseria meningitidis* Z2491 between tufA and pilT, or region 1 of the chromosome, and/or the sequence(s) capable of hybridizing with the above sequence(s), with the proviso of being specific to *Neisseria meningitidis*.

"Specific" in the description and the claims means the nucleotide sequences which hybridize only with those of Nm under the hybridization conditions given in the examples and referred to above.

In this respect, it can be seen that, in a general manner, when "all or part" of a sequence is referred to in the description and claims, this expression must be interpreted with respect to the specificity defined above.

Furthermore, all or part of a peptide or a fragment of a peptide or an antibody means a product having the biological properties respectively of the natural peptide or the antibody formed against the peptide.

Genes of the *Neisseria meningitidis* capsule are grouped in region 1.

DNAs of this type have a sequence corresponding in all or part to SEQ ID No. 9, 13, 22 or 30, and/or to any sequence located at more or less 20 kb from these SEQ ID on the chromosome of an Nm strain, and/or have a sequence which is capable of hybridizing with at least a fragment of any one of these sequences.

In another preferred embodiment of the invention, these DNA are also characterized in that they are made up of one or more sequence(s) present on the chromosome of *Neisseria meningitidis* Z2491 between pilQ and λ740, or region 2 of the chromosome, and/or the sequences(s) capable of hybridizing with the above sequence(s), with the proviso of being specific to *Neisseria meningitidis*.

DNAs according to this embodiment have a sequence corresponding in all or part to SEQ ID No. 1, 2, 4, 6, 7, 10, 15, 31 or 34, and/or to any sequence located at more or less 20 kb from these SEQ ID on the chromosome of an Nm strain, and/or have a sequence which is capable of hybridizing with at least a fragment of any one of these sequences.

The invention especially provides all or part of the DNA sequence SEQ ID No. 36 of 15,620 bp, and the sequences corresponding to the open reading frames SEQ ID No. 37, SEQ ID No. 38, SEQ ID No. 39, SEQ ID No. 40, SEQ ID No. 41, SEQ ID No. 42, SEQ ID No. 43, SEQ ID No. 44 and SEQ ID No. 45.

In yet another preferred embodiment of the invention, these DNAs are also characterized in that they are made up of one or more sequence(s) present on the chromosome of *Neisseria meningitidis* Z2491 between argF and opaB, or region 3 of the chromosome, and/or the sequence(s) capable of hybridizing with the above sequence(s), with the proviso of being specific to *Neisseria meningitidis*.

DNAs according to this embodiment are characterized in that they have a sequence corresponding in all or part to SEQ ID No. 8, 21, 23, 25, 26, 28, 29, 32 or 35, and/or to any sequence located at more or less 20 kb from these SEQ ID on the chromosome of an Nm strain, and/or have a sequence which is capable of hybridizing with at least a fragment of any one of these sequences.

Regions 1, 2 and 3 identified above have a high proportion of sequences specific to *Neisseria meningitidis* and also fall within the context of the invention.

Other DNAs representative of the specificity with respect to *Neisseria meningitidis* have one or more sequences which

is/are present on the chromosome of *Neisseria meningitidis* Z2491 but are not part of regions 1, 2 and 3 defined above.

Such DNAs comprise one or more sequence(s) corresponding in all or part to SEQ ID No. 3, 5, 11, 12, 14, 16, 18, 19, 20, 24, 27 or 33, and/or to any sequence located at more or less 20 kb from these SEQ ID on the chromosome of an Nm strain, and/or have a sequence capable of hybridizing with such sequences.

Taking into account the uses envisaged in particular, the invention more specifically relates to the above DNAs involved in the pathogenesis of the bacterial organism.

In particular, it provides the DNAs corresponding to at least one of the characterizations given above and coding for a protein exported beyond the cytoplasmic membrane, and/or of which all or part of their sequence corresponds to the conserved region of the said DNAs.

According to another embodiment of the invention, the DNAs are thus common with those of Ng, but are absent from those of Nl.

These are more specifically the DNAs which are present on region 4 (arg J to reg F) or on region 5 (lambda 375 marker to pen A) on the chromosome of Nm Z2491 and/or are capable of hybridizing with the said DNAs present, with the proviso of being specific to Nm and Ng, in contrast to Nl.

"Specific to Nm and Ng in contrast to Nl" means the DNAs which hybridize with the DNAs of Nm and Ng under the hybridization conditions of the examples (see example 4 in particular).

The DNAs of regions 4 and 5 and those capable of hybridizing with these DNAs, with the proviso of expressing the intrinsic functions of Nm, have the advantage of intervening in a significant manner in the virulence of Nm, being involved in the stage of initial colonization and penetration and in the septicaemic dissemination.

According to other embodiments, the invention provides transfer and expression vectors, such as plasmids, cosmids or bacteriophages, comprising at least one DNA as defined above.

It also provides host cells transformed by at least one DNA as defined above.

Other host cells of the invention comprise genes or gene fragments specific to Nm, and are characterized in that their chromosome is deleted by at least one DNA according to the invention, in particular a DNA responsible for the pathogenicity. They are more specifically bacterial cells, in particular of Nm.

The invention also relates to the RNAs of which the sequence corresponds in all or part to the transcription of at least one DNA sequence or sequence fragment as defined above.

The invention also relates to the antisense nucleic acids of the DNAs as defined above, or of fragments of these DNAs.

These antisense nucleic acids carry, where appropriate, at least one substituent, such as a methyl group and/or a glycosyl group.

Other products which fall within the context of the invention include polypeptides.

These polypeptides are characterized in that they have an amino acid chain corresponding to all or part of a sequence coded by the nucleic acids defined above, or deduced from sequences of these nucleic acids.

They are advantageously polypeptides corresponding to all or part of the polypeptides exported beyond the cytoplasmic membrane, more specifically polypeptides corresponding to all or part of those coded by a conserved region.

As a variant, the polypeptides of the invention can be modified with respect to those corresponding to the nucleic acid sequences such that they are particularly suitable for a given use, in particular use as a vaccine.

Modification is understood as meaning any alteration, deletion or chemical substitution where this does not affect the biochemical properties of the corresponding natural polypeptides, more specifically of functional proteins exported at the periplasm and the external membrane.

Other products according to the invention include antibodies directed against the above polypeptides.

The invention thus provides polyclonal antibodies, and also monoclonal antibodies, characterized in that they recognize at least one epitope of a polypeptide as described above.

It also relates to fragments of these antibodies, more particularly the fragments Fv, Fab and Fab'2.

The invention also relates to the anti-antibodies which are capable of recognizing the antibodies defined above, or their fragments, by a reaction of the antigen-antibody type.

According to the invention, the various products considered above are obtained by a synthesis and/or biological route in accordance with conventional techniques.

The nucleic acids can also be obtained from banks made up of Nm-specific DNAs such as are formulated by a subtractive technique, this technique comprising:

- mixing of two DNA populations,
- realization of at least one subtractive hybridization-amplification iteration, and
- collection of the desired DNA or DNAs, followed, where appropriate, by its/their purification with elimination of redundant sequences.

According to the invention, the two DNA populations originate respectively from a strain of *Neisseria meningitidis*, the so-called reference strain for which the specific bank must be constructed, and a strain of *Neisseria*, the so-called subtraction strain, having a homology in primary DNA sequences of greater than about 70% with the *Neisseria meningitidis* strain, the DNA sequences of the subtraction and reference strains being obtained respectively by random shearing, and by cleavage by a restriction endonuclease capable of producing fragments less than about 1 kb in size.

The invention provides in particular a process for obtaining *Neisseria meningitidis*-specific DNA banks, comprising the stages of

- random shearing of the chromosomal DNA of a strain of *Neisseria gonorrhoeae*, the so-called subtraction strain, in particular by repeated passage through a syringe,
- cleavage of the chromosomal DNA of a strain of *Neisseria meningitidis*, the so-called reference strain, preferably by a restriction enzyme producing fragments less than about 1 kb in size,
- splicing of the DNA fragments of the reference strain, cleaved by the restriction enzyme, with suitable oligonucleotide primers,
- realization of a subtractive hybridization-amplification iteration, by:
  - mixing of the two DNA populations under suitable conditions for hybridization of homologous sequences, and then
  - amplification of auto-reannealed fragments and collection of these fragments,
  - digestion of these fragments by a restriction enzyme and re-splicing with oligonucleotide primers, followed by a
- purification of the spliced DNA and, where appropriate, a new iteration of the subtractive hybridization, compris-

ing mixing of DNA fragments of *Neisseria gonorrhoeae* sheared as indicated above with DNA fragments of *Neisseria meningitidis* produced by the preceding iteration, followed, if desired, by cloning of the DNAs of the bank.

The primers used are oligodeoxynucleotide primers which are suitable for the restriction endonuclease used and allow insertion into a cloning site, such as the EcoRI site of the plasmid pBluescript. Such primers will advantageously be chosen among the oligodeoxynucleotides referred to in the sequence listing under SEQ ID no. 36 to 45.

The banks thus obtained are formed from DNAs which are specific to meningococci and absent from gonococci.

The specificity of the DNAs was verified, as described in the examples, at each iteration by Southern blots, with genes common to the subtraction strain and to the reference strain, or with the total DNA of each of the strains digested by a restriction endonuclease, such as ClaI.

At each iteration, the exhaustivity of the DNA bank was also verified by Southern blotting with probes known to be specific to the reference strain, that is to say for *Neisseria meningitidis* the frp, opc and rotamase genes in particular.

The experiments carried out showed that the banks obtained by the process of the invention are deficient in genes having a significant homology with species of *Neisseria* other than *Neisseria meningitidis*, for example the ppk or pilC1 genes, generally in only 2 or 3 iterations.

If necessary, two routes, which are not exclusive of each other, can be taken.

It is possible to proceed with an $(n+1)^{th}$ iteration using the DNA of iteration n as the DNA population of the reference strain.

As a variant, a second bank independent of the first is constructed, with a restriction enzyme of different specificity to that used in the first bank, for example MboI.

In all cases, it is preferable to keep each of the products produced by each of the iterations performed.

The invention also provides the use of the subtractive technique described above to obtain banks of the DNAs common to Nm and Ng, but specific with respect to Nl.

Three different banks are advantageously constructed, two of them by digestion of the chromosomal DNA of Nm by MboI and Tsp5091, and the third by digestion of the chromosomal DNA of Nm with MspI. Two subtraction series allow the DNAs having the required specificity to be collected, as described in the examples.

The invention also relates to the process for obtaining these banks and the banks themselves.

It can be seen that, generally, the process of the invention can be used to obtain banks of DNAs specific to a given cell species, or to a given variant of the same species, where another species or another variant which is close genomically and expresses different pathogenic potencies exists.

Using the process of the invention, DNA banks specific to given species of *cryptococci, Haemophilus, pneumococci* or also *Escherichia coli*, or more generally any bacterial agent belonging to the same species and having different pathovars will advantageously be constructed.

Furthermore, from these banks the invention provides the means to have available virulence factors specific to a species or a given variant.

Such banks are therefore tools which are of great interest for having available attributes which are responsible for the specificity of a pathogen, this use being more specifically illustrated according to the invention by the obtaining of banks comprising the attributes responsible for the specificity of the meningococcal pathogenesis.

Study of the products of the invention, the nucleic acids, polypeptides and antibodies, has enabled an absolute specificity with respect ot *Neisseria meningitidis*, regardless of the strain and its variability, to be demonstrated.

These products are therefore particularly suitable for diagnosis or prevention of infections and meningitis caused by *Neisseria meningitidis*, whether in adults or children and regardless of the serogroups of the strain in question.

The method for diagnosis, according to the invention, of a meningococcal infection, and more particularly of meningococcal meningitis, by demonstration of the presence of *Neisseria meningitis* in an analytical sample is characterized by the stages of:

bringing into contact a sample to be analysed, that is to say a biological sample or a cell culture, and a reagent formulated from at least one nucleic acid as defined above, if appropriate in the form of a nucleotide probe or a primer, or, as a variant, from at least one antibody or a fragment of an antibody as defined above, under conditions which allow, respectively, hybridization or a reaction of the antigen-antibody type, and

detection of any reaction product formed.

If the reagent is formulated from a nucleic acid, this can be in the form of a nucleotide probe in which the nucleic acid or a fragment of the latter is labelled in order to enable it to be detected. Suitable markers include radioactive, fluorescent, enzymatic or luminescent markers.

As a variant, the nucleic acid is included in a host cell, which is used as the reagent.

In these various forms, the nucleic acid is used as such or in the form of a composition with inert vehicles.

If the reagent is compiled from an antibody, or a fragment of an antibody, this can be labelled for detection purposes. Most generally, a fluorescent, enzymatic, radioactive or luminescent marker is used.

The antibody or the antibody fragment used, which is labelled if appropriate, can be used as such or in the form of a composition with inert vehicles.

The sample used in the stage of bringing the components into contact is a biological sample produced by a mammal, such as cephalorachidian fluid, urine, blood or saliva.

The detection stage is carried out under conditions which allow the reaction product to be demonstrated when it is formed. Conventional means use fluorescence, luminescence, colour or radioactive reactions, or also autoriadography [sic] techniques. It is also possible to quantify the product.

The invention also relates to the labelled products, the nucleic acids and antibodies, as new products.

The method defined above can be used for diagnosis of an immune reaction specific to a meningococcal infection.

The reagent used is thus a polypeptide according to the invention, as coded by the said nucleic acid sequences, corresponding to the natural product or a polypeptide which is modified but has the biological and immunological activity of the corresponding natural polypeptide.

It is advantageously a polypeptide exported beyond the cytoplasmic membrane of *Neisseria meningitidis*, more particularly the part of such a polypeptide corresponding to the conserved region of the DNA.

The invention also relates to kits for carrying out the methods defined above. These kits are characterized in that they comprise:

at least one reagent as defined above, that is to say of the nucleic acid, antibody or polypeptide type,

products, in particular markers or buffers, which enable the intended nucleotide hybridization reaction or immunological reaction to be carried out, as well as use instructions.

The specificity of the products of the invention and their location on the chromosome of *Neisseria meningitidis* Z2491, either grouped in a region and able to be interpreted as pathogenicity islets, or isolated on the chromosome, impart to them a very particular interest for realization of vaccine compositions with a universal purpose, that is to say whatever the strain and the variability which it expresses. These compositions can include in their spectrum other prophylaxes, and can be, for example, combined with childhood vaccines.

The invention thus provides vaccine compositions which include in their spectrum antimeningococcal prophylaxis, intended for prevention of any infection which may be caused by *Neisseria meningitidis*, these compositions being characterized in that they comprise, in combination with (a) physiologically acceptable vehicle(s), an effective amount of polypeptides or anti-antibodies or their fragments as defined above, these products optionally being conjugated, in order to reinforce their immogenicity [sic].

Immunogenic molecules which can be used comprise the poliovirus protein, the tetanus toxin, or also the protein produced by the hypervariable region of a pilin.

As a variant, the vaccine compositions according to the invention are characterized in that they comprise, in combination with (a) physiologically acceptable vehicle(s), an effective amount:

of nucleic acids as defined above,

of transformed host cells as defined above, or

of Nm cells, the chromosome of which has been deleted by at least one DNA sequence according to the invention involved in the pathogenicity of the bacterium. The nucleotide material used is advantageously placed under the control of a promoter of its expression in vivo and synthesis of the corresponding protein. To reinforce the immunogenicity, it is also possible to combine this nucleic material with a DNA or an RNA which codes for a carrier molecule, such as the poliovirus protein, tetanus toxin or a protein produced by the hypervariable region of a pilin.

The vaccine compositions of the inventions can be administered parenterally, subcutaneously, intramuscularly or also in the form of a spray.

Other characteristics and advantages of the invention are given in the examples which follow for illustration thereof, but without limiting its scope.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWING(S)

In these examples, reference will be made to FIGS. **1** to **11**, which show, respectively,

FIGS. **1**A, **1**B, **1**C, **1**D, **1**E, **1**F and **1**G: analysis of the subtractive bank Tsp5091,

FIG. **2**: the distribution of the Nm-specific sequences, in contrast to Ng, on the chromosome of the strain Z2491 (left-hand part) and of Nm-specific sequences, in contrast to Nl (right-hand part),

FIGS. **3**A to **3**C: the reactivity of the clones of the 3 regions of the chromosome according to the invention towards a panel of strains of the genus *Neisseria,*

FIG. **4**: the position in region 2 of the chromosome of Nm of oligonucleotides used as probes,

FIGS. **5**, **6** and **7**: the Southern blots of a panel of strains of the genus *Neisseria*, using parts of region 2 of Nm as probes,

FIGS. **8**A to **8**C: the Southern blots with 3 subtractive banks over a panel of 12 strains of *Neisseria*, and

FIGS. **9**, **10** and **11**: the reactivity of clones of the 3 subtractive banks with respect to Nm, Nl and Ng.

In the examples which follow, the following materials and methods were used:

Bacterial strains—To obtain the subtractive banks, strain Z2491 of Nm (Achtman et al., 1991, *J. Infect. Dis.* 164, 375–382), the strains MS11 (Swanson et al., 1974, *Infect. Immun.* 10, 633–644) and the strains 8064 and 9764 of Nl were used, it being understood that any other strain of the species in question could be used.

In order to verify the specificity of these banks, 6 strains of Nm, 4 strains of Ng, one strain of Nl (*Neisseria lactamica*) and one strain of Nc (*Neisseria cinerea*) were used.

The six strains of Nm are: Nm Z2491 of serogroup A, Nm 8013 of serogroup C (XN collection), Nm 1121, no serogrouping possible (XN collection), Nm 1912 serogroup A (XN collection), Nm 7972 of serogroup A (XN collection) and Nm 8216 of serogroup B (XN collection).

The four strains of Ng are: Ng MS11 (Pasteur Institute, Paris), Ng 403 (Pasteur Institute, Paris), Ng 6934 (Pasteur Institute, Paris), Ng WI (isolated from a disseminated gonococcal infection), Ng 4Cl, Ng 6493 and Ng FA 1090.

The strains of Nl are Nl 8064 and Nl 9764 (XN collection), and that of Nc is Nc 32165 (XN collection).

Molecular Genetics Techniques

Unless indicated otherwise, the techniques and reagents used correspond to those recommended by Sambrook et al (Sambrook et al 1989, Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press). The oligodeoxynucleotides used in this study are:

```
                                                (SEQ ID No.54)
RBAm12,   3' AGTGGCTCCTAG 54
                                                (SEQ IN No.55)
RBam24,   5' AGCACTCTCCAGCCTCTCACCGAG 3';
                                                (SEQ ID No.60)
Jbam12,   3' GATCCGTTCATG 5';
                                                (SEQ ID No.61)
JBAM24,   5' ACCGACGTCGACTATCCATGAACG 3';
                                                (SEQ ID No.56)
REco12,   AGTGGCTCTTAA;
                                  (= RBam 24,SEQ ID NO.55)
REco24,   5' AGCACTCTCCAGCCTCTCACCGAG 3';
                                                (SEQ ID No.62)
JEco12,   GTACTTGCTTAA;
                                                     (= JBam 24)
JEco24,   5' ACCGACGTCGACTATCCATGAACG 3';
                                                (SEQ ID No.64)
NEco12,   AATTCTCCCTCG;
                                               (SEQ ID No.65).
NEco24,   AGGCAACTGTGCTATCCGAGGGAG;
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Transfer to Membranes (Southern Blots)

The transfers to membranes were effected by capillary transfers to positively charged nylon membranes (Boehringer Mannheim). The hybridizations were carried out at 65° C. in a solution comprising NaPi [sic] 0.5 M pH 7.2/EDTA 1 mM/SDS 7%/BSA 1%. The membranes were washed in a solution comprising NaPi [sic] 40 mM pH 7.2/EDTA 1 mM/SDS 1%. The final washing was carried out at 65° C. for 5 min.

The probe frp obtained with oligonucleotides based on the frpA sequence corresponds to 2.4 kb of the 5' end of the gene of the strain Z2491. The opc and rotamase probes corresponding to whole genes are produced from the strain Z2491 using oligonucleotides constructed on the basis of published sequences. The probes pilCl and ppk (polyphosphate kinase) correspond to inserts of the plasmids pJL1 and pBluePPK6001 respectively.

EXAMPLE 1

Construction of Banks of DNAs Present in Nm and Absent from Ng

a. "MboI" Bank

Construction—The DNA of Nm Z2491 was cleaved by the endonuclease MboI and subjected to two iterations of a method called CDA (comprehensive difference analysis) below. This method comprises subtractive hybridization in the presence of excess sheared DNA of Ng MS11 and amplification by PCR of those meningococcal sequences which, since they are absent from or do not have significant homology with the DNA of Ng MS11, could reanneal.

The chromosomal DNA of the strain Ng MS11 is sheared randomly by repeated passage through a hypodermic syringe until fragments of a size ranging from 3 to 10 kb are obtained. These DNA fragments are purified by extraction with phenol.

The chromosomal DNA of the strain Nm Z2491 is itself cleaved by the restriction endonuclease MboI. These DNA fragments (20 μg) are spliced with 10 nmol of annealed oligonucleotides RBam12 and RBam24. The excess primers are removed by electrophoresis over 2% agarose gel of low melting point. The part of the gel containing amplified fragments greater than 200 bp in size is excised and digested by β-agarase. These fragments are purified by extraction with phenol.

To carry out a subtractive hybridization (first iteration), 0.2 μg of the Nm DNA spliced with the RBam oligonucleotides is mixed with 40 μg Ng DNA in a total volume of 8 ml of a buffer EE 3× (a buffer EE 1× is composed of N-(2-hydroxyethyl)piperazine-N'-(3-propanesulphonic acid) 10 mM and EDTA 1 mM, and its pH is 8.0). This solution is covered with mineral oil and the DNA is denatured by heating at 100° C. for 2 min. 2 μl NaCl 5 M are added and the mixture is left to hybridize at 55° C. for 48 h. The reaction mixture is diluted to 1/10 in a preheated solution composed of NaCl and buffer EE, and in then immediately placed on ice.

10 μl of this dilution are added to 400 μl of PCR reaction mixture (Tris.HCl pH 9.0 10 mM; KCl 50 mM; $MgCl_2$ 1.5 mM; Triton X100 0.1%; 0.25 mM of each of the four triphosphate deoxynucleotides; Taq polymerase 50 units per ml). The mixture is incubated for 3 min at 70° C. to complete the ends of the reannealed meningococcal DNA fragments.

After denaturing at 94° C. for 5 min and addition of the oligonucleotide RBam24 in an amount of 0.1 nmol per 100 μl, the hybridizations are amplified by PCR (30 cycles of 1 min at 94° C., 1 min at 70° C. and 3 min at 72° C., followed by 1 min at 94° C. and 10 min at 72° C.; Perkin-Elmer GeneAmp 9600).

The amplified meningococcal fragments are separated from the primers and high molecular weight gonococcal DNAs on gel. They are digested by MboI and the oligonucleotides JBam12 and JBam 24 are spliced to them again. These spliced DNAs are again purified over gel and extracted with phenol.

A second iteration of the subtractive hybridization is carried out on 40 μg of the randomly sheared Ng DNA and 25 ng of the DNA spliced with the JBam oligonucleotides obtained from the first iteration of the subtractive hybridization. During this second iteration, amplification of the auto-annealed Nm DNA is effected with the aid of the oligonucleotide JBam24.

Specificity—In order to confirm their Nm specificity, the amplified sequences after the second iteration of the CDA method are labelled and used as a probe for the DNA digested by ClaI produced from a panel of six strains of *Neisseria meningitidis*, four of *Neisseria gonorrhoeae*, one of *Neisseria lactamica* and one of *Neisseria cinerea*.

The Southern blots obtained show that the amplified sequences resulting from the second iteration of the CDA method have a high reactivity with several bands corresponding to meningococci, and do not have a reactivity with the bands corresponding to the Ng, Nl and Nc strains.

The "MboI" bank thus appears to be Nm-specific.

Exhaustivity—In order to test the exhaustivity of the bank, all the products produced from the first and second iterations of the CDA method and also the initial chromosomal materials of Nm Z2481 [sic] and Ng MS11 are subjected to agarose gel electrophoresis, transferred to a membrane and brought into contact with probes comprising genes known to be meningococcus-specific, that is to say frp, opc and rotamase (Southern blotting).

As a result of these hybridizations, the Nm-specific gene frp is represented in the MboI bank by a fragment of 600 bp, but no activity is observed for the rotamase and opc genes. The MboI bank, although Nm-specific, therefore cannot be considered exhaustive.

Given their high specificity, the fragments produced by the second iteration of the CDA method for the MboI bank can nevertheless be cloned on the BamHI site of the plasmid pBluescript.

A sequence corresponding to any of the Nm-specific genes can be included in the subtractive bank only if it is carried by a restriction fragment of appropriate size. This condition is a function of two factors. Firstly, the probability that the largest fragments are entirely Nm-specific is low. Secondly, even if such fragments existed, they would be under-represented in the bank because of the limitations of the PCR technique, the amplification effectiveness of which decreases with increasing size of the fragments. Fragments greater that about 600 bp in size are not included in the bank. Because of the absence of Mbo fragments of suitable size from the chromosome of Nm Z2491, the rotamase and opc genes cannot be included in the bank. Any enzyme cannot by itself produce a small fragment corresponding to any Nm-specific gene. A second bank was therefore constructed using another restriction enzyme with a different specificity: Tsp509 [sic].

b. "Tsp5091" Bank

Construction—The enzyme Tsp5091 has the advantage of producing fragments of smaller size (less than about 1 kb) than the enzyme MboI.

Tsp509I recognizes the sequence AATT and leaves, projecting at 5', a sequence of 4 bases compatible with EcoRI. The oligonucleotides used are Reco, Jeco and NEco.

The method followed conforms with that followed for construction of the "MboI" bank described above. However, higher quantities of meningococcal DNA were used for the first iteration of the subtractive hybridization in order to compensate for the higher number of fragments of low molecular weight produced by Tsp509I. For the first iteration, 400 ng Nm DNA fragments and, in the second, 25 ng Nm fragments are subjected to subtractive hybridization with 40 μg randomly sheared Ng DNA.

For the construction of this "Tsp509I" bank, as a control, a third iteration of the subtractive hybridization is carried out using 40 μg sheared Ng DNA and 0.2 ng Nm fragments resulting from a digestion by Tsp509I and a resplicing, with NEco adaptors, of the fragments obtained as a result of the second iteration.

Specificity—As described for the previous bank, the product resulting from the second iteration of the CDA method is labelled and used as the probe for a panel of strains of *Neisseria*.

FIG. **1**A illustrates the Southern blot hybridization of products of the second iteration of the CDA method with the DNA digested by ClaI of: Nm in track a, Ng MS11 in track b, Nm 8013 in track c, Ng 403 in track d, Nm 1121 in track e, Ng 6934 in track f, Nm 1912 in track g, Ng WI (strain DGI) in track h, Nm 7972 in track i, Nl 8064 in track j, Nc 32165 in track k, Nm 8216 in track 1.

In contrast to the high reactivity observed with all the Nm strains, a low or no reactivity is observed with the Ng, Nl and Nc strains.

The specificity of the bank was studied earlier by reacting membrane transfers (Southern blots) of the products produced by each of the three iterations of the CDA method with probes corresponding to pilC1 and ppk. These two genes are common to Nm and Ng.

FIG. **1**B shows an agarose gel after electrophoresis of the chromosomes of Nm Z2491 and Ng Ms11, digested by Tsp509 [sic], and products resulting from each of the iterations of the CDA method.

In track a 1 μg of the chromosome of Nm was deposited, in track b 1 μg of that of Ng, in track c 0.15 μg of the products resulting from the first CDA iteration, in track d 0.1 μg of those of the second iteration, in track e 0.05 μg of the third iteration, MW representing the molecular size markers.

FIGS. **1**C and **1**D show gels obtained as described in FIG. **1**B after transfer to the membrane (Southern blots) and hybridization with pilC1 (FIG. **1**C) and ppk (FIG. **1**D).

At the end of the second iteration of the CDA method, the sequences corresponding to the pilC1 and ppk genes are completely excluded from the bank.

Exhaustivity—The exhaustivity of the bank was examined by reacting the products resulting from the subtractive hybridization with the probes corresponding to three Nm-specific genes (frp, rotamase and opc).

These Nm-specific probes react with the amplification products resulting from the first and second iteration of the subtractive hybridization.

FIGS. **1**E, **1**F and **1**G show gels obtained as described in FIG. **1**B after transfer to the membrane (Southern blots) and hybridization with frpA (FIG. **1**E), rotamase (FIG. **1**F) and opc (FIG. **1**G).

However, a third iteration of the subtractive hybridization leads to the loss of Nm-specific sequences, since the fragments which react with the rotamase and opc genes are absent from this third iteration.

In consideration of all these data, it emerges that the products resulting from the second iteration of the CDA method are Nm-specific and also constitute an exhaustive bank of Nm-specific sequences.

The products resulting from this second iteration are cloned at the EcoRI site of the plasmid pBluescript.

The bank produced by Tsp509I is more exhaustive [sic] than the bank produced by MboI, as the theory considerations based on the enzymatic production of smaller restriction fragments would suggest.

In accordance with this aspect, it should be noted that the Tsp509I bank is less redundant than the MboI bank, that is to say it comprises less duplication of clones. 86% of the clones of the Tsp509I bank correspond to distinct sequences, while only 43% of the clones correspond to distinct sequences in the MboI bank (data not shown).

The bank produced by Tsp509I thus constitutes a source of Nm-specific clones.

EXAMPLE 2

Analysis of the Clones of the Subtractive Bank

Cloning and Sequencing of the Nm-Specific DNAs

The DNAs of the subtractive banks are clones at the BamHI (MboI bank) or EcoRI (Tsp509I bank) site of the plasmid pBluescript, and then transformed in DH5α of *E. coli*. The inserts are amplified by PCR carried out on the transformed colonies using the primers M13-50 and M13-40, the latter primer being biotinylated on its 5' end.

Sequencing was carried out on each PCR product after separation of the biotinylated and non-biotinylated strands using the system of Dynabeads M-280 with streptavidin (Dynal, Oslo). The sequences are screened according to their homologies with previously published sequences using the computer programs Blastn and Blastx (NCBI, USA and Fasta).

The PCR products resulting from the transformed bacteria colonies after using the primers M13-40 and M13-50 as described above were labelled by incorporation with random priming of α-^{32}P-dCTP and were used as a probe for the membrane transfers of the chromosomal DNA digested by ClaI of strains Nm Z2491 and Ng MS11, as described above, in order to verify their specificity.

Mapping of Clones on the Chromosome of the Strain Nm Z2491.

The results of studies carried out with 17 clones of the "MboI" bank (designated by the letter B) and 16 clones of the "Tsp5091" bank (designated by the letter E), each of these clones having a unique sequence and being without counterpart in Ng, are reported.

The positions of the DNA sequences corresponding to cloned Nm-specific products were determined with respect to the published map of the chromosome of Nm Z2491 (Dempsey et al. 1995, J. Bacteriol. 177, 6390–6400) and with the aid of transfers to membranes (Southern blots) of agarose gel subjected to pulsed field electrophoresis (PFGE).

The Nm-specific clones are used as probes for a hybridization on membranes (Southern blots) of the DNA of Nm Z2491 digested with enzymes of rare cutting sites, that is to say PacI, PmeI, SgfI, BglII, SpeI NheI and SgfI.

The gels (20×20 cm) were gels of 1% agarose in a buffer TBE 0.5× and were subjected to electrophoresis at 6 V/cm for 36 hours according to pulsation periods varying linearly between 5 and 35 seconds.

The hybridizations on the membrane (Southern blots) were carried out as described above.

The results obtained are shown on FIG. **2**: the reactivity was located by comparison with the positions of the fragments of corresponding size on the published map. The positions of all the genetic markers mapped by Dempsey et al (mentioned above) are visualized with the aid of points on the to linear chromosomal map. The Nm-specific genes disclosed previously are labelled with an asterisk. The two loci called "frp" correspond to the frpA and frpc genes. The "pilC" loci correspond to the pilC1 and pilC2 genes, which are pairs of homologous genes and are not distinguished on the map. The accuracy of the positions of the Nm-specific clones of the invention depends on the overlapping of reactive restriction fragments. On average, the position is +/−20 kb.

This mapping reveals a non-random distribution of the Nm-specific sequences. The majority of the Nm-specific sequences belong to three distinct groups. One of these groups (region 1) corresponds to the position of genes relating to the capsule which have been described previously.

A distinction is made between:

E109, E138, B230 and B323 as being region 1,

B322, B220, B108, B132, B233, B328, E139, E145 as B101 as being region 2, and

B306, E114, E115, E124, E146, E120, E107, E137 and 142 as being region 3.

63% of the sequences identified as specific to meningococci are located inside these three distinct regions.

This grouping contrasts with the distribution of previously disclosed Nm-specific genes (frpA, frpC, porA, opc and the region relating to the capsule).

This prior art would suggest in fact that the Nm-specific genes, with the exception of functional genes relating to the capsule, were dispersed along the chromosome.

Mapping of Nm-specific sequences on the chromosome leads to an unexpected result with regard to the prior art.

The majority of the genetic differences between the meningococcal and gonococcal strains tested are grouped in three distinct regions.

Meningococcal genes relating to the capsule are grouped in region 1.

The function of genes of the other regions is unknown, but homologies with published sequences (table 1) suggest similarities between certain genes of region 3 and bacteriophage transposase and regulatory proteins. No meningococcal virus has been characterized and it is tempting to think that these sequences are of phagic origin. Interestingly, the genome of *H. influenzae* also contains a sequence homologous to that of the Ner regulatory protein of phage Mu, but it is not known if it is a functional gene.

The clone B208 has a high homology (48% identical, 91% homology for 33 amino acids) with a clone of conserved regions field III) in the class of proteins which bind to TonB-dependent ferric siderophors.

The proximity of this clone with the Nm-specific porA genes and the frp genes regulated by iron, and in particular the possibility that it is an Nm-specific receptor protein exposed on the external membrane in itself is a good candidate for further research.

The clone B339 corresponds to the Nm-specific insertion sequence IS1106.

The low homology between the clone B134 and the Aeromonas insertion sequence and also the presence of multiple copies of the clone B134 among the various strains of Nm suggest that it could be a new type of Nm-specific insertion sequence.

The possibility that the regions containing the Nm-specific clones could correspond to pathogenicity islets as described previously for *E. coli* and *Y. pestis* is of particular interest.

The clones isolated in this invention will allow better understanding of the relevance of Nm-specific regions in allowing cloning and sequencing of larger chromosomal fragments, and directly by their use for loci mutations.

Finally, detection of meningococcus-specific genes possibly involved in the pathogenicity of the organism allows targeting of suitable antigens which can be used in an antimeningococcal vaccine.

The effectiveness and the speed of the method according to the inventions enables it to be used in a large number of situations for which the genetic differences responsible for a phenotype peculiar to one of 2 close pathogens are investigated.

Study of the Reactivity of the Clones of Regions 1, 2 and 3 Towards a Panel of Strains of *Neisseria.*

The PCR products corresponding to inserts of each of the clones were collected and used as probes for hybridization on membranes (Southern blots) for a panel of strains of Nm, Ng, Nl and Nc.

Regions 1 and 2 produce a limited number of bands for each of the meningococci. This suggests that these regions are both Nm-specific and common to all the meningococci.

FIG. **3** illustrates the reactivity of the clones of regions 1, 2 and 3 towards a panel of neisserial strains. The clones of regions 1 (FIG. **3**A), 2 (FIG. **3**B) and 3 (FIG. **3**C) taken together were used as probes towards a panel of meningococci, gonococci and towards a strain of Nl and Nc.

The tracks are as follows: DNA of: Nm Z2491 in track a, of Ng MS11 in track b, of Nm 8013 in track c, of Ng 403 in track d, of Nm 1121 in track e, of Ng 6934 in track f, of Nm 1912 in track g, of Ng WI (strain DGI) in track h, of Nm 7972 in track i, of Nl 8064 in track j, of Nc 32165 in track k, and of Nm 8216 in track 1.

Remarkably, region 3 has reactivity only with the meningococci of serogroup A. This region 3 is therefore specific to a sub-group of Nm.

A comparison was made with the known sequences in the databanks in order to evaluate the possible functions of the cloned regions.

Table 1 which follows gives the positions of specific clones on the chromosomal map and the homologies with known sequences.

TABLE 1

Position of specific clones on the chromosomal map and homologies with known sequences

Name of clone*	Size of insert	Reactive fragments						Position on Z2491	Homologies of protein sequences
		Pac	Pmc	Bg1	Spe	Nhe	Sgf		
B305	259	18–20	15–17	22–23	18	11–13	2	λ736	
B333	235		15–17	22–23	18	11–13	2	λ736	
E109[1+]	211		6–7	11–15	10	11–13	2	tufA ctrA	protein LipB *N. meningitidis* (3×10^{-26})

TABLE 1-continued

Name of clone*	Size of insert	Reactive fragments: Pac	Pmc	Bg1	Spe	Nhe	Sgf	Position on Z2491	Homologies of protein sequences
		Position of specific clones on the chromosomal map and homologies with known sequences							
E138[1+]	315	1	6–7	11–15	10	11–13	2	tufA ctrA	protein LipB *N. meningitidis* (4×10^{-75})
B230[1]	356	1–3	6–7	1	10	11–13	2	ctrA	protein KpsC *E. coli* (3×10^{-53})
B323[1]	363	1	6–7	1	10	11–13	2	ctrA	protein CtrB *N. meningitidis* (2×10^{64})
B322[2]	210		2	16–18	6	1	5	pilQ/λ740	HlyB *S. marcescens* (4×10^{-15})
B220[2]	341		2	16–18	6	≧18	5	pilQ/λ740	
B108[2]	275		2	19–21	6	≧18	5	pilQ/λ740	
B132[2]	411	2	2	19–21	6	≧18	5	pilQ/λ740	
B233[2]	164	1–3	2	19–21	6	≧18	5	pilQ/λ740	
B328[2]	256	1–3	2	22–23	6	≧18	5	pilQ/λ740	
E139[2]	324	2	2	19–21	6	≧18	5	pilQ/λ740	
E145[2]	343	2	2	19–21	6	≧18	5	pilQ/λ740	
B101[2]	254	≧20	2	19–21	6	≧18	5	pilQ/λ740	
E103q	334		2	11–15	3–5	10	3	λ644	
B326[§]	314		2	11–15	3–4	10	3	λ644	
B326 (low reactivity)			5	6	16	2	1	argF	
B342	167		2	19	3–4	6–7	3	iga	
E136	249		2	7	1	3	3	lepA	
B208	177		1	2	3–4	2	1	porA	FeIII pyochelin receptor *P. aeruginosa* (5.10^{-4})
= B306[3#]	219	11	5	11–12	5	2	4	parC	
E114[3]	227	11	5	11–12	5	2	4	parC	
E115[3#]	251		5	11–15	5	2	4	parC	
E124[3]	208		5	11–12	5	2	4	parC	
E146[3]	146		5	11–15	5		4	parC	
E120[3]	263		5	3–4	5	16	4	opaB	
E107[3]	248	11	14–17	3–4	5	16	4	opaB	
E137[3]	274		14–17	3–4	5	16	4	opaB	Transposase Bacteriophage D3112 (6×10^{-12})
E142[3]	230		14–17	3–4	5	16	4	opaB	Protein Ner-Likc *H. influenzae* (6×10^{-23}) Protein binding to the DNA Ner, phage mu (3×10^{-18})
E116	379	5–7	11–13	3–4	2	6–7	8	λ375	
B313	436	9	9	3–4	13–14	5	2	λ611	
B341	201	8–10	9	3–4	13–14	5	2	λ611	
E102	238		11–13	3–4	19	5	2	λ601	Hypothetical protein H11730 *H. influenzae* (7×10^{-24})
B134	428			multiple					transposase ISAS2 *Aeromonas salmonicida* (5×10^{-5})
B339	259			multiple					transposase IS 1106 *N. meningitidis* (6×10^{-45})

The level of homologies found, as given by the Blastx program, are indicated in parentheses

*The clones labelled with the index "1", "2" or "3" belong to regions "1", "2" or "3" respectively of the chromosome of *N. meningitidis* Z2491.

[1+]E109 and E138 are contiguous clones [§]B306 and E115 overlap [#]B236 also has a low reactivity in the region of arg F

q) Clone E103 contains a Tsp509 I site and can therefore contain two inserts; however, since it reacts only with a single fragment ClaI (Oks) of the chromosome of *N. meningitidis* Z2491 and occupies only one position on the map, this clone is included here.

Firstly, it can be seen that the clones of region 1 all correspond to genes involved in biosynthesis of the capsule. These genes have previously been studied among the Nm of serogroup B (Frosch et al. 1989, Proc. Natl. Acad. Sci. USA 86, 1669–1673 and Frosch and Muller 1993, Mol. Microbiol. 8 483–493).

With the exception of a low homology with the haemolysin activator of *Serratia marcescens*, the clones of region 2 have no significant homology with published sequences, either in the DNA or the proteins.

Two of the clones of region 3 have interesting homologies with proteins which bind to the DNA, in particular the bacteriophage regulatory proteins and transposase proteins.

Clone B208 has a high homology with one of the conserved regions in one class of receptors (TonB-dependent ferric siderophor).

Clones B134 and B339 hybridize with several regions of the chromosome (at least 5 and at least 8 respectively).

Data relating to the sequences show that clone B339 corresponds to the Nm-specific insertion sequence S1106.

The translation of the clone B143 has a limited homology with the transposase of an *Aeromonas* insertion sequence (SAS2) (Gustafson et al. 1994, J. Mol. Biol. 237, 452–463). We were able to demonstrate by transfer on a membrane (Southern blots) that this clone is an Nm-specific entity present in multiple copies in the chromosomes of every meningococcus of the panel tested.

The other clones have no significant homology with the published neisserial sequences, and furthermore nor with any published sequence. These clones therefore constitute, with the majority of the other clones isolated, a bank of totally new Nm-specific loci.

EXAMPLE 3

Study of Region 2 of the Nm Chromosome

Determination and Characterization of the Sequence of Region 2

PCR amplification is carried out with the chromosomal DNA of strain Z2491 of serogroup A, sub-group IV-1 using oligonucleotide primers formulated from each of the sequences of clones of region 2 in several different combinations. The PCR products which overlap are sequenced from the 2 strands using the chain termination technique and automatic sequencing (ABI 373 or 377).

To prolong the sequence beyond the limits of the clones available, partial SauIIIA fragments of 15 kb of the strain Z2491 are cloned in Lambda DASH-II (Stratagene).

The phages containing the inserts overlapping region 2 are identified by hybridization with clones of this region as probes. The DNA inserted is sequenced from the ends of the inserts, and these sequences are used to formulate new primers which will serve to amplify the chromosomal DNA directly, and not the phagic DNA.

An amplification of the chromosomal DNA is obtained using these new primers and those of the sequence previously available.

These PCR products are also sequenced from the 2 strands, which leads to a complete sequence of 15,620 bp (SEQ ID No. 36). The reading frames of this sequence which start with ATG or GTG and are characterized by a high codon usage index are analysed.

This analysis reveals 7 ORFs of this type which fill the major part of the sequence of 15,620 bp. The positions of these ORFs are the following:

ORF-1: 1330 to 2970 (SEQ ID No. 37); ORF-2: 3083 to 9025 (SEQ ID No. 38); ORF-3: 9044 to 9472 (SEQ ID No. 39); ORF-4: 9620 to 12118 (SEQ ID No. 40); ORF-5: 12118 to 12603 (SEQ ID No. 42); ORF-6: 12794 to 13063 (SEQ ID No. 43); ORF-7: 13297 to 14235 (SEQ ID No. 44); and ORF-8: 14241 to 15173 (SEQ ID No.45).

ORF-4 starts with the codon GTG and overlaps a slightly smaller ORF (SEQ ID No. 41) in the same reading frame (10127–12118, frame 2), which starts with the codon ATG.

ORF-4 codes for a protein which has structural homologies with a family of polypeptides comprising pyocins (*Pseudomonas aeruginosa*), collcins and intimins (*Escherichia coli*), which are bactericidal toxins (pyocins, collcins) or surface proteins involved in adhesion of bacteria to eukaryotic proteins. ORF-7 encodes a protein, the sequence of which contains a potentially transmembrane region and which has structural homologies with periplasmic proteins or proteins inserted in the external membrane of bacteria. The structural homologies of ORF-4 and ORF-7 have been identified with the aid of the PropSearch program.

Investigation of sequences homologous to other ORFs in GenBank with the aid of the BLAST program revealed a homology between the N-terminal regions of ORF-2 and filamentous haemagglutinin B of *Bordetella pertussis* (43% similarity, 36% identical over 352 amino acids) and between ORF-1 and the protein fhaC of *Bordetella pertussis* (35% similarity, 27% identical over 401 amino acids). ORF-1 and ORF-2 are neighbouring genes in the strain Z249I and filamentous haemagglutinin B of *Bordetella pertussis* and fhaC are neighbouring genes in *Bordetella pertussis*, which reinforces the probability that these homologies reflect functional homologies.

Confirmation of the specificity of region 2 with respect to Nm

Southern blots are carried out using the DNA probes obtained by PCR amplification of various parts of region 2 using oligonucleotide primers formulated from sequences of clones of region 2.

The approximate position of these oligonucleotides is shown on FIG. **4**.

These are the oligonucleotides called R2001 (SEQ ID No. 46) and R2002 (SEQ ID No. 47) in one half of ORF-1, the oligonucleotides b332a (SEQ ID No. 48), e139a (SEQ ID No. 49), b132a (SEQ ID No. 50) and b233b (SEQ ID No. 51) in one half of ORF-1+the majority of ORF-2, and the oligonucleotides e145a (SEQ ID No. 52) and b101a (SEQ ID No. 53) in ⅓ of ORF-4+ORF-5 to 7.

The three Southerns are carried out under the following hybridization conditions:

16 h at 65° C.,

$NaPO_4$ 0.5 M, pH 7.2

EDTA-Na 0.001 M

1% sodium dodecylsulphate.

For the washing, heating is carried out for 10 min at 65° C., and $NaPO_4$ 0.5 M, pH 7.2; EDTA-Na 0.001 M, 1% sodium dodecylsulphate are used.

FIGS. **5**, **6** and **7** respectively show the Southern blots obtained with each of the abovementioned ORF parts.

The 14 tracks correspond respectively, in each of the Southerns, to

1: MS11 (Ng)
2: 403 (Ng)
3: FA1090 (Ng)
4: W1 (Ng)
5: 6493 (Ng)
6: marker (lambda hindIII)
7: Z2491 (Nm, gpA)
8: 7972 (Nm gpA)
9: 8013 (Nm, gpC)
10: 1121 (Nm, grouping not possible)

11: 1912 (Nm, gpB)
13: 32165 (Nc)
14: 8064 (Nl).

Given that a panel of strains of *Neisseria* is used in these experiments and that each well is charged with a similar amount of digested DNA, these 3 Southern blots clearly show that the sequences corresponding to region 2 are found in all the meningococci tested and that significant homologous sequences do not exist in the genome of the Ng of the strains tested.

EXAMPLE 4

Identification of Regions of the Nm Genome Absent from Nl and Common with Ng

The technique described in example 1 is followed, but the chromosomal DNA of one strain of Nm (Z2491) and 2 strains of Nl (XN collections), equal parts of the DNAs of which are mixed, is used.

2 subtractions are performed using the R and J series of primers. Three different banks are thus obtained.

Two banks, called Bam and Eco, are obtained respectively by digestion of the chromosomal DNA of Nm Z2491 by MboI and Tsp5091; a third bank, called Cla, which results from digestion of the chromosomal DNA of Nm by MspI, is obtained using the primer set RMsp10, RMsp24, JMsp10 and JMsp24. All the primers used are shown in the following table 2.

TABLE 2

Adapters for differential banks

Chromosomal DNA digested by	Cloning in pBluescript by
MboI →	BamHI
Tsp509I →	EcoRI
MspI →	ClaI

First subtraction cycle

(SEQ ID No.54)
RBam12: 3' AGTGGCTCCTAG 5'
(SEQ ID No. 55)
RBam24: 5' AGCACTCTCCAGCCTCTCACCGAG 3'
(SEQ ID No.56)
REco12: AGTGGCTCTTAA
(SEQ ID No. 55)
RBam24: 5' AGCACTCTCCAGCCTCTCACCGAG 3'
(REco 24 = RBam 24)
(SEQ ID No.57)
RMsp10: AGTGGCTGGC
(SEQ ID No. 58)
RMsp24: 5' AGCACTCTCCAGCCTCTCACCGAC 3'

Second subtraction cycle

(SEQ ID No.59)
Jbam12: 3' GTACTTGCCTAG 5'
(SEQ ID No. 60)
JBam24: 5' ACCGACGTCGACTATCCATGAACG 3'
(SEQ ID No. 61)
JEco12: GTACTTGCTTAA
(SEQ ID No 60)
JBam24: 5' ACCGACGTCGACTATCCATGAACG 3'
(JEco 24 = TBam 24)
(SEQ ID No. 62)
JMsp10: GTACTTGGGC
(SEQ ID No. 63)
JMsp24: 5' ACCGACGTCGACTATCCATGAACC 3'

After 2 subtractions, the entire product of each amplification is labelled and used as a probe.

The subtractive banks are checked by Southern blotting over a panel of 12 strains of *Neisseria* (chromosomal DNA cut by ClaI). The hybridization conditions are identical to those given in example 1.

These Southern blots are shown on FIGS. **8**A to **8**C, which relate respectively to the MboI/BamHI bank, to the MspI/ClaI bank and to the Tsp5091/EcoRI bank.

The 12 tracks correspond respectively, to
1: Nm Z2491 (group A)
2: Nl 8064
3: Nm 8216 (group B)
4: Nl 9764
5: Nm 8013 (group C)
6: Ng MS11
7: Nm 1912 (group A)
8: Ng 4C1
9: Nm 1121 (grouping not possible)
10: Ng FAlO9O
11: Nc 32165
12: Nm 7972 (group A)

Examination of the Southern blots shows that the sequences contained in each bank are specific to Nm and are not found in Nl. Furthermore, the reactivity found with the strains of Ng suggests that some of these sequences are present in Ng.

Each of these banks was then cloned in pBluescript at the BamHI site for Bam, or the EcoRI sit for Eco, or the ClaI site for Cla. In order to confirm the specificity of the clones with respect to the Nm genome, restriction of the individual clones and radiolabelling thereof were carried out. The clones showing reactivity for both Nm and Ng were kept for subsequent studies. These clones are shown on FIGS. **9**, **10** and **11**, which give the profiles with respect to Nm, Nl and Ng of 5 clones of the Bam bank (FIG. **9**), 16 clones of the Eco bank (FIG. **10**) and 13 clones of the Cla bank (FIG. **11**).

These clones were sequenced using universal and reverse primers. They are

Bam clones

partial B11 of 140 bp (SEQ ID No. 66), partial B13 estimated at 425 bp (SEQ ID No. 67), B26 of 181 bp (SEQ ID No. 68), B33 of 307 bp (SEQ ID No. 69), B40 of 243 bp (SEQ ID No. 70),

Cla clones

C16 of 280 bp (SEQ ID No. 72), partial C20 estimated at 365 bp (SEQ ID No. 73), partial C24 estimated at 645 bp (SEQ ID No. 74), partial C29 estimated at 245 bp (SEQ ID No. 75), C34 of 381 bp (SEQ ID No. 76), C40 of 269 bp (SEQ ID No. 77), C42 of 203 bp (SEQ ID No. 78), p C43 of 229 bp (SEQ ID No. 79), C45 of 206 bp (SEQ ID No. 80), C47 of 224 bp (SEQ ID No. 81), C62 of 212 bp (SEQ ID No. 82), and C130 (5' . . .) estimated at 900 bp (SEQ ID No. 83), and

Eco clones

E2 of 308 bp (SEQ ID No. 84), partial E5 estimated at 170 bp (SEQ ID No. 85), partial E22 estimated at 300 bp (SEQ ID No. 86), E23 of 273 bp (SEQ ID No. 87), E24 of 271 bp (SEQ ID No. 88), E29 of 268 bp (SEQ ID No. 89), partial E33 estimated at 275 bp (SEQ ID No. 90), partial E34 estimated at 365 bp (SEQ ID No. 91), E45 of 260 bp (SEQ ID No. 92), E59 estimated at greater than 380 bp (SEQ ID No. 93), E78 of 308 bp (SEQ ID No. 94), E85 of 286 bp (SEQ ID No. 95), E87 of 238 bp (SEQ ID No. 96), partial E94 greater than 320 bp (SEQ ID No. 97), partial E103 greater than 320 bp (SEQ ID No. 98) and E110 of 217 bp (SEQ ID No. 99).

Mapping of each clone was carried out on the chromosome of Nm Z2491 as described in example 1. The results obtained are given on the right-hand part of FIG. **2**. It is

found that these clones correspond to regions called 4 and 5. These regions are therefore made up of sequences present both in Nm and in Ng, but not found in Nl. It is therefore regarded that these are sequences which code for virulence factors responsible for the initial colonization and penetration of the mucosa. Region 4 is located between argF and regF on the chromosome of Nm 2491 [sic], and region 5 is located between the lambda 375 marker and penA. This region probably contains sequences which code for an Opa variant and a protein which binds transferrin.

A comparison with the known sequences in the databanks has half [sic] that in region 4 only the clone C130 has a homology, that is to say with MspI methylase. In region 5, no homology with known sequences was found with the clones C8, E2, B40, C45, E23 and E103. For the other clones, the homologies are the following:

B11 arginine decarboxylase SpeA; C29 arginine decarboxylase SpeA; C62 oxoglutarate/malate transporter; repetitive DNA element; E34 repetitive DNA element; E94 murine endopeptidase MepA; C47 citrate synthase PrpC; E78 citrate synthase PrpC

EXAMPLE 5

Demonstration of the Presence of One or More Strains of *Neisseria meningitidis* in a Biological Sample

A biological sample of the cephalorachidian fluid, urine, blood or saliva type is taken.

After filtration and extraction, the DNAs present in this sample are subjected to gel electrophoresis and transferred to a membrane by Southern blotting.

A nucleotide probe constructed by labelling SEQ ID No. 5 with ^{32}P is incubated with this transfer membrane.

After autoradiography, the presence of reactive band(s) allows diagnosis of the presence of *Neisseria meningitidis* in the sample.

EXAMPLE 6

Vaccine Composition Including in its Spectrum Antimeningococcal Prophylaxis and Intended for Prevention of any form of Infection by *Neisseria meningitidis*

The peptide coded by a sequence including SEQ ID No. 10 is conjugated with a toxin.

This conjugated peptide is then added to a composition comprising the anti-*Haemophilus* and antipneumococcal vaccine, or any other childhood vaccine.

After having been sterilized, the resulting composition can be injected parenterally, subcutaneously or intramuscularly.

This same composition can also be sprayed on to mucosa with the aid of a spray.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 99

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GATCCGCTGC CGGCAGACGA ATATCAAGAC ATCTTCGATT TTATGAAACA GTATGACTTG 60

TCTTACCCGT ATGAATATCT GCAGGATTGG ATAGATTACT ATACGTTCAA AACCGATAAG 120

CTGGTATTTG GTAACGCGAA GCGAGAGTGA GCCGTAAAAC TCTGAGCTCC TGTTTTATAG 180

ATTACAACTT TAGGCCGTCT TAAAGCTGAA AGATTTTCGA AAGCTATAAA TTGAAGCCCT 240

TCCACAGTAC ATAGATC 257

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single

-continued

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GATCATGTTC AAATAGATAG GCATGGGAAG CTGCAGCTCT AACGTCCATG AAAATATGTT 60

GCATAGCTGC AAGCGGAACG CCTTTTCTTT CATCTACATA ATCTATAGAG TCAAGGCAAC 120

CGCTATTGAA ATTAGCAGTA TTGCCTATGA TTACATTAGT AATATGCTCA TACCATTTTT 180

GGGTGGTCAT CATATTGTGC CCCATTGTTA TCTCCTTATA TTGGTTTTAG AAGGAACTTT 240

GACAGGAAGA ATAACGGCCT TACCTGTTTG ACGATC 276

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 428 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GATCTGGTGG TGTTTGCACA GGTAGGCGCA TACTTGTTCG GGACTGAGTT TGCGGCGGAT 60

AAGGGTGTCG ATGTGCTGAA TCAGCTGCGA ATCGAGCTTA TAGGGTTGTC GCTTACGCTG 120

TTTGATAGTC CGGCTTTGCC GCTGGGCTTT TTCGGCGCTG TATTGCTGCC CTTGGGTGCG 180

GTGCCGTCTG ATTTCGCGGC TGATGGTGCT TTTGTGGCGG TTAAGCTGTT TGGCGATTTC 240

GGTGACGGTG CAGTGGCGGG ACAGGTATTG GATGTGGTAT CGTTCGCCTT GGGTCAGTTG 300

CGTGTAGCTC ATGGCAATCT TTCTTGCAGG AAAGGCCGTA TGCTACCGCA TACTGGCCTT 360

TTTCTGTTAG GGAAAGTTGC ACTTCAAATG CGAATCCGCC GACCTCTTTC AGTTACAGCA 420

GCTTGATC 428

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATCCTGCAT TGACATCGGC CTTGGCTGTC AGGGTATTGT GACCGGTAAA GTCGGCATTA 60

CCGTTGGCCA ATAAGGATAC ATGACCGTCT GCAGAAACAG CATGAAGGCC GTCTGAAACG 120

ATATTGCCCT GCAATGCGGT GGTTTCGAGA GCCTTGGCTG CGTTCAGCTT GGTATTGCGA 180

AGCTGAATAT TGCCTTTGGC TGCCTGAATG TGCAGATTAC CCGAGTTGGT ACGCAGATTG 240

GTATTGGTAA CATTCAGCAA GCCTGCCTCC ACACCCATGT CTTTTGAGGC AGTGAGGGTT 300

-continued

TTACTGGTGC CGGTAATATG GCAGCGTTA TCCGATTTCA AATGGATGCT GGCCGGCAGA 360

CAAATCTTTA TCAACATTCA AATTCAGATC 390

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GATCAGATTG GTGAAGACGG TATTACCGTC AATGTTGCAG GCCGTTCGGG ATATACGGCG 60

AAAATCGACG TGTCTCCGAG TACCGATTTG GCGGTTTATG GCCATATTGA AGTTGTACGG 120

GGTGCAACGG GGTTGACCCA ATCCAATTCA GAGCCGGGTG GAACCGTCAA TTTGATC 177

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GATCAATGAT GCTACTATTC AAGCGGGCAG TTCCGTGTAC AGCTCCACCA AAGGCGATAC 60

TGAATTGGGT GAAAATACCC GTATTATTGC TGAAAACGTA ACCGTATTAT CTAACGGTAG 120

TATTGGCAGT GCTGCTGTAA TTGAGGCTAA AGACACTGCA CACATTGAAT CGGGCAAACC 180

GCTTTCTTTA GAAACCTCGA CCGTTGCCTC CAACATCCGT TTGAACAACG GTAACATTAA 240

AGGCGGAAAG CAGCTTGCTT TACTGGCAGA CGATAACATT ACTGCCAAAA CTACCAATCT 300

ACTCCC GGCAATCTGT ATGTTCATAC AGGTAAAGAT C 341

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GATCCAACTG TTTGATTTTA CTGGCTGCTT CTCCATGCGC GGTATTGACC AAAGCCGCAA 60

GGATATTCGC TTCCAGATTG TCTTTCAGGC TGCCGCCGTT GACAGCGGTA TTAATCAGTG 120

CGGCACTGCC CGCATTGGCT AGGTTGACGG TCAGGTTGTT GATC 164

-continued

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATCAATCAC ACATCTTGTC ATTTTTTCGA TTCCTTCATT TCGGTTTCTA ATGTTTCAAT 60

TCTTGCGGCC ATTTCCTGAA TGGCTTTAGT CAAAACGGGG ATGAACGCTT CGTATTCGAC 120

GGTGTAGGTA TCGTTTGTTT TATTTACCAT CGGCAATCGA CCATATTCAT CTTCCAGCGC 180

AGCAATGTCC TGGGCAATAA ACCAATGCCG CAACCGATC 219

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATCTTGGGT AAGCCCCCAA CCTGCATAGA AAGGCAGGCC GTAGCAGCTG ACTTTTTTGC 60

CGCGCAACAA GGCTTCAAAA CCGGTCAGCG AAGTCATGGT ATGTATTTCG TCTGCGTATT 120

GGAGACAGGT CAGGATGTCG GCTTGTTCGG CGGTTTGGTC GGCATATCGT GCAGCATCAT 180

CAGGGGAAAT ATGGCCGATG CGGTTACCGC TGACTACATC GGGATGCGGT TTGTAGATGA 240

TATAGGCATT GGGGTTTCGT TCGCGTACGG TACGGAGCAA ATCCAGATTG CGGTAGATTT 300

GGGGCGAACC GTAGCGGATA GACGCATCAT CTTCAACCTG GCCGGGAACG AGGATC 356

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GATCCGCTTT CAGTTTCCGT ACCGGTGGCA TCAGTCAAGT CCGTTTTGTG CACCAAACCG 60

CGTCCATATG AAACATAAAA CAAATCGCTT AAGCCCAAAG GGTTATCGAA CGATAAAGCG 120

ACATTTCCTT GATATTTGCC GGTCGTTTTG CCGCCCGCAT CATCTATACC GATACTGAAC 180

CGTATGGGTT TATTCTGCTG CCATTTGATC 210

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(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GATCCCGAAA CGCAATTGGT CGAAAGCTAT ATGCTGAACG ATGTGTTGCG GTTTTGGGAC 60

AGCGCAGGTT TGGGCGATGG GAAAGAAGCC GACCGCGCCC ATCGGCAAAA ACTGATTGAT 120

GTCCTGTCTA AAACCTATAC TCATTCGGAT GGGCAGTGGG GCTGGATAGA TTTGGTGTTC 180

GTTATCCTTG ACGGCAGCTC CCGCGATTTG GGTACGGCCT ATGATTTGTT GAGGGATGTT 240

ATCCTTAAAA TGATTGATC 259

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GATCAAATGG ATGATTTATA TAGAATTTTC TTTTACGACT GCGTGCCGTT TGAAAAGAAA 60

ATGCACAATC CCGTATCTCA TCGTGCCATA GATTTTTCAA AGACTCCGGA AGCCATATTT 120

CGTTGCAATC TGCATACCGA ATTGAAGAAG AAGCGTAAAT TAGCGTTACG TTTAGGCAAG 180

CTGTCGGACA ATACAGCATG GATATTAAAA CCCCAAGTCA TGAAAAATCT TCTGAAAAAC 240

CCGTCAACTC AAATTACGGA AAACGATGTC GTGCTCGATG TTAAACAAAA AGGTGTAGAT 300

ATGCGTATAG GCTTGGATAT TTCATCTATT ACCTTAAAAA AACAAGCCGA TAAAATCATC 360

TTGTTTTCTG GTGATTCCGA TTTTGTCCCA GCAGCCAAAT TAGCCAGACG GGAAGGTATC 420

GATTTTATTC TTGATC 436

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GATCGTTTTA CGTCGCAATC GAGCTTTGTG GTGCGCTCGC CTAAAAGCCA ATCTTCTCTC 60

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AATGGCCTGG GTGCCATTTT GCAGGGCACA GGTTTTGCCC GTGCGCAAGA CGATATTTAT 120

ACCGTGCAGG AATATATGCA GTCGCGTTCG GCTTTGGATG CGTTGCGTAA GAAAATGCCC 180

ATTCGCGATT TTTATGAAAA AGAAGGCGAT ATTTTCAGCC GTTTTAATGG TTTTGGCCTG 240

CGTGGCGAGG ATGAGGCGTT TTATCAATAC TACCGTGATA AGGTATCCAT CCATTTTGAC 300

TCTGTCTCAG GCATTTCCAA TTTGAGCGTT ACATCGTTTA ATGCCGGTGA ATCTCAAAAG 360

ATC 363

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GATCTTGCGT CATTTATATC TTCACCGATA TTGCAATTAC CGCCGTTCCA GTTGAAATAA 60

CAACGACTAA AATTGTAGTT CCTAAAAGAA TCATTCCTAT TCTTGCGTAC CATTTCCCAA 120

TAATTGCGCC CGACAATTTC CATTTAATGC TCCATCAGTT CTTTTACTTC CGGAAATCTG 180

CTGTAATCTG ACATAAGACG CATAATTGAA CTATCAACGC CGTAACAGCC ATAGGTTTTA 240

ATACCGTTTT CGGCGTGTTC CCAAATGCAA TTACTGTATT CGTAGCCTTT TACAAATTTA 300

TCGGTTTCGG GATC 314

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCATACGA ATCTACCCTA AAATACCCCG TCGCCGATTT AGGATTGGCT ACATAAAGCT 60

CATTATAAGG GTATTTTGAT GACATGATAC GGTTAAATTC ATTGCCGTTG TTTATCCTGA 120

TTCTATAAAT TGGTTCAACA GCAAAGCCTC TGGATTCCCT TAATTGATTA TAATATTGCC 180

TGTATGTTTG TACATCATGT CTTGTCCACG GCTCTCCAGG AGTCCTCAGA ATAGCAATCC 240

CGTTAAATTT CGGATC 256

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GATCCACGCC TGTGCCTACC TTGGCTTTTT GTTCGCCAAA CAAGGCATTT AAGGTTGAGG 60

ACTTGCCGAC ACCTGTCGCA CCGACAAGCA AGACATCCAA ATGACGGAAA CCGGCTGCTG 120

TGACTTTTTG CCCGATTTCA GAAATACGGT AACGATGCAT ATGCGCTCCT ACCAGCCAAA 180

AAAAGAAGCA ACCGTGCTAA TCGCCCCTCC AATCGCTTTT GCAGCACCGC CGATC 235

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GATCCAACGG GCATCGCTGT CCTTACTCGG TGTGGTTTGA CCGCTGATTT GTCCTTCTTC 60

GTCAACTTCT ATGGCCTGAC GCTGTTTGCT GCCGGCGGTC TGGATAATGG TGGCATCAAC 120

GACGGCGGCG GATGCTTTCT CTATTTTTAG GCCTTTTTCG GTCAGTTGGC AGTTAATCAG 180

TTTGAGTAAT TCGGACAGGG TGTCGTCTTG CGCCAGCCAG TTGCGGTAGC GGCATAAGGT 240

ACTGTAATCG GGGATGATC 259

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GATCTGTGCC GTTGATTTTA TCTTTCAGAT GCAGCATCGA ATATCGGAAA GCCAAATCAG 60

CAATTCTTTT TGCATCGTGT GGATTTTGAG ACGGGCCTAA TGACCGTACC CGCTTAATAA 120

AAAATGCACC GTCAATCAAA ATGGCGGTTT TCATATTGCT TCCCCTATAT TTGTCAAAGA 180

TATAAAAAAG CCCTTGGGAT C 201

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AATTCAAAGG AGGCATTTGT TGCAAGAAAA GTACAAAGTG ATTTGCAAAA AGCATTGAAT 60

GCTAGCAACT ATAACAAGCA GCAATATGCA AGACGTGCGG CAACAGCGTT AGAGAATGCT 120

TCAAAATCAA AAGTTATGGC AGCGAATTCT TTTTGATCTA TCTTGTGCGA ACGGGTCAAA 180

TATTCTTCGT ACATTGAGTT AATCGTACCA ATCGCCCTAA CCACATTTTC ATCAGAAAAT 240

ATGGAAATAA TAGCATCCCT ATACGCACCT AGTGTAATAT TGTTTCTATT ATTAGTTATA 300

GCATTATTCG AATACATAAT AGCACCTCCA AATT 334

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AATTCCTGCG CACCTTTGCC GATGGGGAGA TAATCGCCTT TTTGCAGCAT TCTGCCCTGA 60

TGGCCGCCGA AACCGGCTTT CAGGTCGGTA CTTCTCGAAC CCATCACTTC CGGCACATCA 120

AATCCGCCCG CCACGCACAC ATAGCCGTAC ATGCCCTGCA CGGCACGCAC CAGTTTCAAG 180

GTCTGCCCTT TGCGGGCGGT ATAACGCCAA TACGAATAGA CCGGTTCGCC GTCCAATT 238

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

AATTGGGCGA GATGCTGCCG GAAACGGATT TAAAACAGAT TGCGGCGGCA GTGTTGAAGA 60

CGAACGATGA GGCGGCATTG CAGAAGGTGG TGAAAACGGC CAAAGGCAAT GCGCGGAAAC 120

TGTCGAAGCT GCTGCTGATT GTGGACTATT TGTTGCAGGT TAACCCTGAT GTTGATTTGG 180

ATGATGATGT AATCGAACAC GCGGAAACCT ATTTAATCCA CTAAACCTTT GACAGATAAG 240

GCAATAATT 249

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AATTTATGTA CGGTTTTGCC GTTTGCAGTC AGCCAGTCGG CAAGGCGCAG AAAAAAATCG 60

CCGACAGGGC CTTGAAGCAG CAGGATATTT TCTGCGCTTT CAAGCAGGTT TTGCAGGTTA 120

TTTTTGAGGA CGGTCTGTTT CATGTTGCAA TGTGGTTTTG TTTTTTATGT AATAGTTTTA 180

GGTTGAACTT TCAAGCATAC GCCAAGAGAA TT 212

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AATTCAGTGC CTGCGTCATA TCACGGCTAC CTTGTGGTTC AGGGTTACTG TATCGCCCGC 60

GGCATCGACG GCTTCAATAT GCAGCTTCAG CCAGCCGTGC TGCGGGGCGG ATGCGGTTAC 120

TTGGATGGAT TGGGCGCGTT TGGACTGAAT CACGGGCTGC AAGGCTTGCT CGGCGTACTG 180

TTTGGCCAGT ACTTCGATGC GCTTTAAATG CTTTTGGCGG CGCAATT 227

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GATCCAGGAC TCAAAAACCG ATTTCCTAAT AGAGTGTCTA ATATCCCAAT CTTTTTTACC 60

CCCTCTGCTG TAGAATTGAT AGAGAAAGTT TGTCTATCTT TTTCATATAC CCATGCCTTC 120

TTTTTATCAT TGTAGCTAAC ATAACCGCCA AACAATGCTT CTAGATC 167

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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AATTCTTGCG GCCATTTCCT GAATGGCTTT AGTCAAAACG GGGATGAACG TTTCGTATTC 60

GACGGTGTAG GTATCGTTTG TTTTATTTAC CATCGGCAAT CGACCATATT CATCTTCCAG 120

CGCAGCAATG TCCTGGGCAA TAAACCAATG CCGCAACCGA TCTTCTTTAT GACTGCCGTC 180

CTTGATTGGA TTCGCCCACC ATTCGCGGAC TTTGTCCGCT CGTTCATCTG CCGGCAAGTC 240

TTTGAATAAT T 251

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

AATTCCCGAC TATCGCGGAT GCGTAGTTTT TGCCGGTGGG CAAGAGCAGG TGTGGGATAA 60

GTTAGGTGAT TTGCCCGATG GCGTCAGCCT GACCCCGCCT GAATCGGTAA ATATTGACGG 120

CTTAAAATCC GTAAAACTCG TCGCATTAAA TGCTGCCGCT CAGGCTTTTA TTAACAAGCA 180

CGCCGGTATC GACAGCGTAC CTGAATT 207

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

AATTGTTTGG GAATAATCCA AACAAACAGC ATCAGGATAG CGGCGGCGGT CAGGCTGCCT 60

GAAAGGATTT TGCCGGGGTT TTTTGTAGGC AAAGCGGACG AGAAACCAAA GCAACAGCAG 120

CATGGTGTCC CAATAGCCGA TTGAGAATAG GATGGCCAAA CCTTCTAGGA AATGGCGTAA 180

ATCGTTTGTG GTAACCATGG GTAGTTCCTG TGGTTAAATG TGCAGGCTGC TTTTTGCCGA 240

ACCTTGCCGC ATCTCAAAAG CAGCCTGCGC TTCAGCGTTG CGTTACGCAG TAAAATAATG 300

AATATTTGTA ACGGCTTGGG TATTTTTTGT CAATATTCCC GCCCTTCCCT TAACAGCTGC 360

CGCGCTTTCC GTTAAAATT 379

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

-continued

(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

AATTCGCCGA AATCAGGCTG CTGCTCGATA ATCGGCGCGG CCGATTGGCG TTGTGCCTCG 60

ATTAAATCCA TCTTGTCTTG CAGACGTTTG GCCTGGCCTT TGCGGCGGCG TTCGGCCAGT 120

TGTTCCATCC GCGTTTCCGC AAATGCCGCC CGTTTGTTGC CGTTGAATAC CGCTTTGCAA 180

ATCACCTTGC CCTGCATATC CTTCACAATC ACATGGTCGG CATCGTGGAT GTCGTAAGCC 240

ACCCGTACCT TCTGACCGCT GTAATCCAGC AATT 274

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AATTCCGTTC TTATTGGGCT TTTTCCATCC ATCGGGTATG CCTGAAGGGA ACGCAAACCC 60

TGCCACTTGC CCATCGCTCC ATTCCCGCAT TAGCGCGTCT GACGGCAAGT GTTCTCGCGC 120

CCAATCAAGC CACGCCTGCC GCATTGCGGC CTTGTCCTGC TGAAAACTTC GCAGTGCTTT 180

TGCAACCGGC CCATCATTAA CTTCAATCAA ATAAATCATT ATATTTGCGT TCATTTTTCC 240

TACACCTTCG CCACATCCAA ATT 263

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

AATTGTTCAA GAAAAAAGTC GGCACGGCGC GGCAACGGGG AAAATGCGTT GACGCCGTCT 60

TTTTCTAAGG TGATGTAGTA GGGGCGGAAA TAGCCTTCTT CAAACGCCCA GAAACTGGCT 120

TGGTTTTCGT TTGCAATGCG TTTTGCAATG ACGTGATAAG GGCGTGTGTC GCCAAAGCAG 180

ACAACGGCCT GGATGTGATG TTGAGTGATG TATTCTTGCA AAAACTCAGG AAAGGCGTCG 240

TAGTTGTCGT TAAAAACAAC GGTATGCGCT TGAGTGGGCG GATAAAAATA GTCGTCGCCT 300

GCATTAAAGT TGAATT 316

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AATTCAATCA ACGGAAAACA CATCAGCATC AAAAACAACG GTGGTAATGC CGACTTAAAA 60

AACCTTAACG TCCATGCCAA AAGCGGGGCA TTGAACATTC ATTCCGACCG GGCATTGAGC 120

ATAGAAAATA CCAAGCTGGA GTCTACCCAT AATACGCATC TTAATGCACA ACACGAGCGG 180

GTAACGCTCA ACCAAGTAGA TGCCTACGCA CACCGTCATC TAAGCATTAC CGGCAGCCAG 240

ATTTGGCAAA ACGACAAACT GCCTTCTGCC AACAAGCTGG TGGCTAACGG TGTATTGGCA 300

CTCAATGCGC GCTATTCCCA AATT 324

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AATTATGCAA AAAAACGCAA CGCCGAAAAA CTGGCACCGC GCGGATATTG TTGCTGCTTT 60

GAAAAAGAAA GGCTGGTCAC TTCGAGCACT TTCAATAGAA GCGGGGTTGT CGCCGAATAC 120

GCTTAGAAGC GCACTGGCCG CCCCTTATCT TAAGGGAGAA AGGATTATTG CCGCTGCAAT 180

CGGAGTGGAA CCGGAAGAGA TTTGGTCCGA ACGGTATGCA GATCGGAATT 230

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

AATTTAATCG GTGGAATGCC TGTTCAACCG CACCAATCCC GCTGAATACG GTTGCTAATC 60

TAATATGTGA ATCAGGTTTA AGAAAAGTTT TAGATTTCCA ACCTTGTTGA CTGGGAAAGA 120

GCAAAGTTTT TTGTAATCGA GTATCGTGTG TCTGTGCCAT TGTCGAAATA GTCATACTTA 180

TATCGTTCTG TTTATCTTAT CAATATGAAA ACTACATCGT TGATTGCCCT GACAATGCCT 240

TGGTCAATT 249

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleotide

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AATTCTTGTC CCGGAGTCCA ACGTATATTT ACCCTCCTGC GAGCTAAAAG ACTATTATTC 60

TCCACTGCCA CAGTAGCCGC ATTCACCGCC GTATTCACAT CCCCTTTAAC CAATGCCACT 120

GCGCTGCCTG CGATAATCTG CGAGTAGGCT ATGACTTTTT GGCGTTCTTG GGGTGACAGT 180

TTGCCTACAT CGCGTCCGTC CAACAGGGTT TCTCCCACCA TCTCGCCGAC TGCCGCGCCG 240

ATTGCGCCGT CCCGACATTT GCCTTTATTT GCTACCGCCG ATGCACAGCC TGCTACGGCA 300

TGGGCTATCT TGTGGGCAAT GTAGTCTTCG CTGAGATTAA ATT 343

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AATTCTTCAA ACATCGTTTC GATAATCGGG TCGGTGTACA CACTGATGCG GTCGCCCGCA 60

CGGCTTTGAC CGGCTCGGAA AATATAGGCG GTGGCTTTGC CGTCGGCGAT GTCGACGCAC 120

CAACGCCAGA TGGCGTCTTC GGTATTCAAA CAATCACCCG CACAGCTTTC ACCTGCGCGG 180

AATT 184

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15620 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria meningitidis
(B) STRAIN: Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TATGCTCAAT CTCATTTTCA AAATGCAAAA CTTTTCTGAT TTTTCCTACT TTTTGCTCAA 60

TATTAGGAAG GTTTTAGGCA ATTGAAAATT TTTTGGCGCA TTTTTATGCG TCAAATTTCG 120

TTAACAGACT ATTTTTGCAA AGGTCTCCGT CTGTAAAAGC AAGGATAGGG CATCTGCCCT 180

TTTGATTGTT TGATTAACGA TACAAGGAGT TTCAAAATGA GAGTTTTATA GTGGATTAAC 240

AAAAACCAGT ACAGCGTTGC CTCGCCTTGC CGTACTATTT GTACTGTCTG CGGCTTCGTC 300

GCCTTGTCCT GATTTAAATT TAATCCACTA TATGTGTTCA TGAAATGACT TGGGTCGGAG 360

GCTCAGGTAA TGCGCAACAA AGTTCATATT ATTGCGAAAT TTGCGAATCT GCAGGGCTTA 420

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ACGATACGGG AAATCCTGAT AAATCTTTAG GATTGCCAAA CAATACGTTC AGTAATCCGC    480

CTGGTTGGGG AGCTACAATC GGAGCTTTAG CAGGTAGCCG CATAGGTATG CCTGAATTTG    540

GTACGTTTGC GAGCCATGCC ATTGAAAATT TCGACTGGTC ATGGTATCGA CGTTATAGGG    600

AAATTGCCGA AACGATTGAA CGAGAATATT CAGGCGGTTT GCCTTAATAG TTGAGGAGGT    660

CATGATGTTT GCCAAACATT ATCAATTCAT CGCACTCGGC ATCATGCTGC TTCTTTATAT    720

GTTGATTCTC TATACGACCG ATTTTTCCAA TCTGACGTAT TGGATGCTGT TTTTTATCTG    780

TTTTATTACA GGAAAAATAT TAGCTCGTTT GTTAGAGAAA AGCTTTAAAT AAAATAGCAG    840

CTAGTCGCAA AAGGTCGTCT GAAACCTTTT CAGGCGGCCT TTCTAAAATA CATCCAACTT    900

CCTAATCCCT ATTTTTCAAA AAGGAAATCT ATGCCCCATC TGCAAAACCT GTCTTTGGGC    960

TTAAAGAAAA AGCTGCCTGT TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT   1020

CTGGCGGCTG TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA   1080

TACTGTCCGA GACCTTTGCA AAATTCCCCA AAATCCCCTA AATGTCTTGG TGGGAATTTT   1140

GGGGAATTTT GCAAAGGTCT CATTCTATAA CTGTAAATAC TTTTAAATTT ATGACAAAAT   1200

AGTAAATATT GCTAAAATAA TATTGATGTC ATGAAATTTT TTCCTGCTCC ATGTCTGTTG   1260

GTTATCCTGG CTGTCATACC CCTTAAAACC TTAGCTGCCG ATGAAAACGA TGCAGAACTT   1320

ATCCGTTCCA TGCAGCGTCA GCAGCACATA GATGCTGAAT TGTTAACTGA TGCAAATGTC   1380

CGTTTCGAGC AACCATTGGA GAAGAACAAT TATGTCCTGA GTGAAGATGA AACACCGTGT   1440

ACTCGGGTAA ATTACATTAG TTTAGATGAT AAGACGGCGC GCAAATTTTC TTTTCTTCCT   1500

TCTGTGCTCA TGAAAGAAAC AGCTTTTAAA ACTGGGATGT GTTTAGGTTC CAATAATTTG   1560

AGCAGGCTAC AAAAAGCCGC GCAACAGATA CTGATTGTGC GTGGCTACCT CACTTCCCAA   1620

GCTATTATCC AACCACAGAA TATGGATTCG GGAATTCTGA AATTACGGGT ATCAGCAGGC   1680

GAAATAGGGG ATATCCGCTA TGAAGAAAAA CGGGATGGGA AGTCTGCCGA GGGCAGTATT   1740

AGTGCATTCA ATAACAAATT TCCCTTATAT AGGAACAAAA TTCTCAATCT TCGCGATGTA   1800

GAGCAGGGCT TGGAAAACCT GCGTCGTTTG CCGAGTGTTA AAACAGATAT TCAGATTATA   1860

CCGTCCGAAG AAGAAGGCAA AAGCGATTTA CAGATCAAAT GGCAGCAGAA TAAACCCATA   1920

CGGTTCAGTA TCGGTATAGA TGATGCGGGC GGCAAAACGA CCGGCAAATA TCAAGGAAAT   1980

GTCGCTTTAT CGTTCGATAA CCCTTTGGGC TTAAGCGATT TGTTTTATGT TTCATATGGA   2040

CGCGGTTTGG TGCACAAAAC GGACTTGACT GATGCCACCG GTACGGAAAC TGAAAGCGGA   2100

TCCAGAAGTT ACAGCGTGCA TTATTCGGTG CCCGTAAAAA AATGGCTGTT TTCTTTTAAT   2160

CACAATGGAC ATCGTTACCA CGAAGCAACC GAAGGCTATT CCGTCAATTA CGATTACAAC   2220

GGCAAACAAT ATCAGAGCAG CCTGGCCGCC GAGCGCATGC TTTGGCGTAA CAGGTTTCAT   2280

AAAACTTCAG TCGGAATGAA ATTATGGACA CGCCAAACCT ATAAATACAT CGACGATGCC   2340

GAAATCGAAG TGCAACGCCG CCGCTCTGCA GGCTGGGAAG CCGAATTGCG CCACCGTGCT   2400

TACCTCAACC GTTGGCAGCT TGACGGCAAG TTGTCTTACA AACGCGGGAC CGGCATGCGC   2460

CAAAGTATGC CCGCACCTGA AGAAAACGGC GGCGGTACTA TTCCAGGCAC ATCCCGTATG   2520

AAAATCATAA CCGCCGGATT GGATGCAGCG GCCCCGTTTA TGTTGGGCAA ACAGCAGTTT   2580

TTCTACGCAA CCGCCATTCA AGCTCAATGG AACAAAACGC CTTTGGTTGC CCAAGACAAG   2640

TTGTCTATCG GCAGCCGCTA CACCGTTCGC GGATTTGATG GGGAGCAGAG TCTTTTCGGA   2700

GAGCGAGGTT TCTACTGGCA GAATACTTTA ACTTGGTATT TTCATCCGAA CCATCAGTTC   2760

TATCTCGGTG CGGACTATGG CCGCGTATCT GGCGAAAGTG CACAATATGT ATCGGGCAAG   2820
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CAGCTGATGG GTGCAGTGGT CGGCTTCAGA GGAGGGCATA AAGTAGGCGG TATGTTTGCT   2880

TATGATCTGT TTGCCGGCAA GCCGCTTCAT AAACCCAAAG GCTTTCAGAC GACCAACACC   2940

GTTTACGGCT TCAACTTGAA TTACAGTTTC TAACCTCTGA ATTTTTTTAC TGATATTTAG   3000

ACGGTCTTTC CTTATCCTCA GACTGTCAAA CTTTACCTAC GTACTTGGCG CGCAGTACGT   3060

TCATCTTCAA AATGGAATAG ACATGAATAA AGGTTTACAT CGCATTATCT TTAGTAAAAA   3120

GCACAGCACC ATGGTTGCAG TAGCCGAAAC TGCCAACAGC CAGGGCAAAG GTAAACAGGC   3180

AGGCAGTTCG GTTTCTGTTT CACTGAAAAC TTCAGGCGAC CTTTGCGGCA AACTCAAAAC   3240

CACCCTTAAA ACCTTGGTCT GCTCTTTGGT TTCCCTGAGT ATGGTATTGC CTGCCCATGC   3300

CCAAATTACC ACCGACAAAT CAGCACCTAA AAACCAGCAG GTCGTTATCC TTAAAACCAA   3360

CACTGGTGCC CCCTTGGTGA ATATCCAAAC TCCGAATGGA CGCGGATTGA GCCACAACCG   3420

CTATACGCAG TTTGATGTTG ACAACAAAGG GGCAGTGTTA AACAACGACC GTAACAATAA   3480

TCCGTTTCTG GTCAAAGGCA GTGCGCAATT GATTTTGAAC GAGGTACGCG GTACGGCTAG   3540

CAAACTCAAC GGCATCGTTA CCGTAGGCGG TCAAAAGGCC GACGTGATTA TTGCCAACCC   3600

CAACGGCATT ACCGTTAATG GCGGCGGCTT TAAAAATGTC GGTCGGGGCA TCTTAACTAT   3660

CGGTGCGCCC CAAATCGGCA AAGACGGTGC ACTGACAGGA TTTGATGTGC GTCAAGGCAC   3720

ATTGACCGTA GGAGCAGCAG GTTGGAATGA TAAAGGCGGA GCCGACTACA CCGGGGTACT   3780

TGCTCGTGCA GTTGCTTTGC AGGGGAAATT ACAGGGTAAA AACCTGGCGG TTTCTACCGG   3840

TCCTCAGAAA GTAGATTACG CCAGCGGCGA AATCAGTGCA GGTACGGCAG CGGGTACGAA   3900

ACCGACTATT GCCCTTGATA CTGCCGCACT GGGCGGTATG TACGCCGACA GCATCACACT   3960

GATTGCCAAT GAAAAAGGCG TAGGCGTCAA AAATGCCGGC ACACTCGAAG CGGCCAAGCA   4020

ATTGATTGTG ACTTCGTCAG GCCGCATTGA AAACAGCGGC CGCATCGCCA CCACTGCCGA   4080

CGGCACCGAA GCTTCACCGA CTTATCTCTC CATCGAAACC ACCGAAAAAG GAGCGGCAGG   4140

CACATTTATC TCCAATGGTG GTCGGATCGA GAGCAAAGGC TTATTGGTTA TTGAGACGGG   4200

AGAAGATATC AGCTTGCGTA ACGGAGCCGT GGTGCAGAAT AACGGCAGTC GCCCAGCTAC   4260

CACGGTATTA AATGCTGGTC ATAATTTGGT GATTGAGAGT AAAACTAATG TGAACAATGC   4320

CAAAGGCTCG GCTAATCTGT CGGCCGGCGG TCGTACTACG ATCAATGATG CTACTATTCA   4380

AGCGGGCAGT TCCGTGTACA GCTCCACCAA AGGCGATACT GAATTGGGTG AAAATACCCG   4440

TATTATTGCT GAAAACGTAA CCGTATTATC TAACGGTAGT ATTGGCAGTG CTGCTGTAAT   4500

TGAGGCTAAA GACACTGCAC ACATTGAATC GGGCAAACCG CTTTCTTTAG AAACCTCGAC   4560

CGTTGCCTCC AACATCCGTT TGAACAACGG TAACATTAAA GGCGGAAAGC AGCTTGCTTT   4620

ACTGGCAGAC GATAACATTA CTGCCAAAAC TACCAATCTG AATACTCCCG GCAATCTGTA   4680

TGTTCATACA GGTAAAGATC TGAATTTGAA TGTTGATAAA GATTTGTCTG CCGCCAGCAT   4740

CCATTTGAAA TCGGATAACG CTGCCCATAT TACCGGCACC AGTAAAACCC TCACTGCCTC   4800

AAAAGACATG GGTGTGGAGG CAGGCTTGCT GAATGTTACC AATACCAATC TGCGTACCAA   4860

CTCGGGTAAT CTGCACATTC AGGCAGCCAA AGGCAATATT CAGCTTCGCA ATACCAAGCT   4920

GAACGCAGCC AAGGCTCTCG AAACCACCGC ATTGCAGGGC AATATCGTTT CAGACGGCCT   4980

TCATGCTGTT TCTGCAGACG GTCATGTATC CTTATTGGCC AACGGTAATG CCGACTTTAC   5040

CGGTCACAAT ACCCTGACAG CCAAGGCCGA TGTCAATGCA GGATCGGTTG GTAAAGGCCG   5100

TCTGAAAGCA GACAATACCA ATATCACTTC ATCTTCAGGA GATATTACGT TGGTTGCCGG   5160
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CAACGGTATT CAGCTTGGTG ACGGAAAACA ACGCAATTCA ATCAACGGAA AACACATCAG   5220

CATCAAAAAC AACGGTGGTA ATGCCGACTT AAAAAACCTT AACGTCCATG CCAAAAGCGG   5280

GGCATTGAAC ATTCATTCCG ACCGGGCATT GAGCATAGAA AATACCAAGC TGGAGTCTAC   5340

CCATAATACG CATCTTAATG CACAACACGA GCGGGTAACG CTCAACCAAG TAGATGCCTA   5400

CGCACACCGT CATCTAAGCA TTACCGGCAG CCAGATTTGG CAAAACGACA AACTGCCTTC   5460

TGCCAACAAG CTGGTGGCTA ACGGTGTATT GGCACTCAAT GCGCGCTATT CCCAAATTGC   5520

CGACAACACC ACGCTGAGAG CGGGTGCAAT CAACCTTACT GCCGGTACCG CCCTAGTCAA   5580

GCGCGGCAAC ATCAATTGGA GTACCGTTTC GACCAAGACT TTGGAAGATA ATGCCGAATT   5640

AAAACCATTG GCCGGACGGC TGAATATTGA AGCAGGTAGC GGCACATTAA CCATCGAACC   5700

TGCCAACCGC ATCAGTGCGC ATACCGACCT GAGCATCAAA ACAGGCGGAA AATTGCTGTT   5760

GTCTGCAAAA GGAGGAAATG CAGGTGCGCC TAGTGCTCAA GTTTCCTCAT TGGAAGCAAA   5820

AGGCAATATC CGTCTGGTTA CAGGAGAAAC AGATTTAAGA GGTTCTAAAA TTACAGCCGG   5880

TAAAAACTTG GTTGTCGCCA CCACCAAAGG CAAGTTGAAT ATCGAAGCCG TAAACAACTC   5940

ATTCAGCAAT TATTTTCCTA CACAAAAAGC GGCTGAACTC AACCAAAAAT CCAAAGAATT   6000

GGAACAGCAG ATTGCGCAGT TGAAAAAAAG CTCGCCTAAA AGCAAGCTGA TTCCAACCCT   6060

GCAAGAAGAA CGCGACCGTC TCGCTTTCTA TATTCAAGCC ATCAACAAGG AAGTTAAAGG   6120

TAAAAAACCC AAAGGCAAAG AATACCTGCA AGCCAAGCTT TCTGCACAAA ATATTGACTT   6180

GATTTCCGCA CAAGGCATCG AAATCAGCGG TTCCGATATT ACCGCTTCCA AAAAACTGAA   6240

CCTTCACGCC GCAGGCGTAT TGCCAAAGGC AGCAGATTCA GAGGCGGCTG CTATTCTGAT   6300

TGACGGCATA ACCGACCAAT ATGAAATTGG CAAGCCCACC TACAAGAGTC ACTACGACAA   6360

AGCTGCTCTG AACAAGCCTT CACGTTTGAC CGGACGTACG GGGGTAAGTA TTCATGCAGC   6420

TGCGGCACTC GATGATGCAC GTATTATTAT CGGTGCATCC GAAATCAAAG CTCCCTCAGG   6480

CAGCATAGAC ATCAAAGCCC ATAGTGATAT TGTACTGGAG GCTGGACAAA ACGATGCCTA   6540

TACCTTCTTA AAAACCAAAG GTAAAAGCGG CAAAATCATC AGAAAAACCA AGTTTACCAG   6600

CACCCGCGAC CACCTGATTA TGCCAGCCCC CGTCGAGCTG ACCGCCAACG GTATCACGCT   6660

TCAGGCAGGC GGCAACATCG AAGCTAATAC CACCCGCTTC AATGCCCCTG CAGGTAAAGT   6720

TACCCTGGTT GCGGGTGAAG AGCTGCAACT GCTGGCAGAA GAAGGCATCC ACAAGCACGA   6780

GTTGGATGTC CAAAAAAGCC GCCGCTTTAT CGGCATCAAG GTAGGTAAGA GCAATTACAG   6840

TAAAAACGAA CTGAACGAAA CCAAATTGCC TGTCCGCGTC GTCGCCCAAA CTGCAGCCAC   6900

CCGTTCAGGC TGGGATACCG TGCTCGAAGG TACCGAATTC AAAACCACGC TGGCCGGTGC   6960

CGACATTCAG GCAGGTGTAG GCGAAAAAGC CCGTGTCGAT GCGAAAATTA TCCTCAAAGG   7020

CATTGTGAAC CGTATCCAGT CGGAAGAAAA ATTAGAAACC AACTCAACCG TATGGCAGAA   7080

ACAGGCCGGA CGCGGCAGCA CTATCGAAAC GCTAAAACTG CCCAGCTTCG AAAGCCCTAC   7140

TCCGCCCAAA TTGTCCGCAC CCGGCGGCTA TATCGTCGAC ATTCCGAAAG GCAATCTGAA   7200

AACCGAAATC GAAAAGCTGT CCAAACAGCC CGAGTATGCC TATCTGAAAC AGCTCCAAGT   7260

AGCGAAAAAC ATCAACTGGA ATCAGGTGCA GCTTGCTTAC GACAGATGGG ACTACAAACA   7320

GGAGGGCTTA ACCGAAGCAG GTGCGGCGAT TATCGCACTG GCCGTTACCG TGGTCACCTC   7380

AGGCGCAGGA ACCGGAGCCG TATTGGGATT AAACGGTGCG GCCGCCGCCG CAACCGATGC   7440

AGCATTCGCC TCTTTGGCCA GCCAGGCTTC CGTATCGTTC ATCAACAACA AAGGCGATGT   7500

CGGCAAAACC CTGAAAGAGC TGGGCAGAAG CAGCACGGTG AAAAATCTGG TGGTTGCCGC   7560
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CGCTACCGCA GGCGTAGCCG ACAAAATCGG CGCTTCGGCA CTGAACAATG TCAGCGATAA 7620

GCAGTGGATC AACAACCTGA CCGTCAACCT AGCCAATGCG GGCAGTGCCG CACTGATTAA 7680

TACCGCTGTC AACGGCGGCA GCCTGAAAGA CAATCTGGAA GCGAATATCC TTGCGGCTTT 7740

GGTCAATACC GCGCATGGAG AAGCAGCCAG TAAAATCAAA CAGTTGGATC AGCACTACAT 7800

AGTCCACAAG ATTGCCCATG CCATAGCGGG CTGTGCGGCA GCGGCGGCGA ATAAGGGCAA 7860

GTGTCAGGAT GGTGCGATAG GTGCGGCTGT GGGCGAGATA GTCGGGGAGG CTTTGACAAA 7920

CGGCAAAAAT CCTGACACTT TGACAGCTAA AGAACGCGAA CAGATTTTGG CATACAGCAA 7980

ACTGGTTGCC GGTACGGTAA GCGGTGTGGT CGGCGGCGAT GTAAATGCGG CGGCGAATGC 8040

GGCTGAGGTA GCGGTGAAAA ATAATCAGCT TAGCGACAAA GAGGGTAGAG AATTTGATAA 8100

CGAAATGACT GCATGCGCCA AACAGAATAA TCCTCAACTG TGCAGAAAAA ATACTGTAAA 8160

AAAGTATCAA AATGTTGCTG ATAAAAGACT TGCTGCTTCG ATTGCAATAT GTACGGATAT 8220

ATCCCGTAGT ACTGAATGTA GAACAATCAG AAAACAACAT TTGATCGATA GTAGAAGCCT 8280

TCATTCATCT TGGGAAGCAG GTCTAATTGG TAAAGATGAT GAATGGTATA AATTATTCAG 8340

CAAATCTTAC ACCCAAGCAG ATTTGGCTTT ACAGTCTTAT CATTTGAATA CTGCTGCTAA 8400

ATCTTGGCTT CAATCGGGCA ATACAAAGCC TTTATCCGAA TGGATGTCCG ACCAAGGTTA 8460

TACACTTATT TCAGGAGTTA ATCCTAGATT CATTCCAATA CCAAGAGGGT TTGTAAAACA 8520

AAATACACCT ATTACTAATG TCAAATACCC GGAAGGCATC AGTTTCGATA CAAACCTAAA 8580

AAGACATCTG GCAAATGCTG ATGGTTTTAG TCAAGAACAG GGCATTAAAG GAGCCCATAA 8640

CCGCACCAAT TTTATGGCAG AACTAAATTC ACGAGGAGGA CGCGTAAAAT CTGAAACCCA 8700

AACTGATATT GAAGGCATTA CCCGAATTAA ATATGAGATT CCTACACTAG ACAGGACAGG 8760

TAAACCTGAT GGTGGATTTA AGGAAATTTC AAGTATAAAA ACTGTTTATA ATCCTAAAAA 8820

ATTTTCTGAT GATAAAATAC TTCAAATGGC TCAAAATGCT GCTTCACAAG GATATTCAAA 8880

AGCCTCTAAA ATTGCTCAAA ATGAAAGAAC TAAATCAATA TCGGAAAGAA AAAATGTCAT 8940

TCAATTCTCA GAAACCTTTG ACGGAATCAA ATTTAGATCA TATTTTGATG TAAATACAGG 9000

AAGAATTACA AACATTCACC CAGAATAATT TAAAGGAAAA ATTATGAAAA ATAATATTTT 9060

TCTAAACTTA AATAAAAAAT CTATAAATAA CAACCATTTT GTTATTTCGA TTTTTTTTGA 9120

AACAATTTAC CAATTTGAAA CTAAAGATAC GCTTTTAGAG TGTTTTAAAA ATATTACAAC 9180

TACCGGACAT TTTGGAGTAA TAGGTGCTCA ATATGAAAAA ATAGATGCTA CCAGATGGAT 9240

TGGAGATTAT GAAGAGGTAA ATGGATTTGA GTATATTGAT AAAGCTCCTT CTATTTATTT 9300

TTCAGTTGGA GATGATTTCA ATCCTGAAGA ATTAATTATA CCTATTAATT TAGCATATCA 9360

TTACTTTAAT ATTGCAATAT CTGATTTCTT AATAGCTCAC CCTGAATATC AAAAAAAGTG 9420

TAAAGAAATA CAAAAAACAT ATTCTCAAAC AAACTGTAGC CTGCATGAAA CCTAAAATCC 9480

ATGCGTAAGG TGTGTGCTTC AGCACGCACG CGTTCCATGA TTTACGGCTC AATGCCGTCT 9540

GAAAAGCTCA CAATTTTTCA GACGGCATTT GTTATGCAAG TAAATATTCA GATTCCCTAT 9600

ATACTGCCCA GACGCGTGCG TGCTGAAGAC ACCCCCTACG CTTGCTGCAG AACTTTCGGG 9660

TAAAACCGGT GTGAGCATTA GCGCACCGTA TGCCAATGAG AACAGTCGCA TCCTGCTCAG 9720

CACCACGGAT ATCAGTTCGG AAAACGGCAA AATCAAAATT CAATCTTACG GTGACCAATA 9780

TTACTATGCG AGACAGAGCG AACTCTATAC CTTTGAACGC CGCAGCTACA AAACTGGCAA 9840

ATGGTACAAC CGCAAACACA TTACCGAAGT CAAAGAACAC AAAAACGCCA AGCCCGACGC 9900

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AGTAAACCTC AGCGCATCCC AAGGCATCGA CATCAAATCT GGTGGCAGCA TCGACGCCTA   9960

CGCCACCGCA TTCGATGCCC CCAAAGGCAG CATTAACATC GAAGCCGGGC GGAAATTGAC  10020

ACTCTATGCC GTAGAAGAGC TCAACTACGA CAAACTAGAC AGCCAAAAAA GGCGCAGATT  10080

TCTCGGCATC AGCTACAGCA AAGCACACGA CACCACCACC CAAGTCATGA AAACCGCGCT  10140

GCCCTCAAGG GTAGTTGCAG AATCAGCCAA CCTCCAATCG GGCTGGGATA CCAAACTGCA  10200

AGGCACACAG TTTGAAACCA CACTGGGTGG CGCAACCATA CGCGCAGGCG TAGGTGAGCA  10260

GGCACGGGCA GATGCCAAGA TTATCCTCGA AGGGATCAAA AGCAGCATCC ACACAGAAAC  10320

CGTGAGCAGC AGCAAATCTA CTCTATGGCA AAAACAGGCA GGACGGGGCA GTAACATCGA  10380

AACCTTGCAA TTGCCGAGTT TCACCGGTCC CGTTGCGCCC GTACTGTCCG CACCCGGCGG  10440

TTACATTGTC GACATTCCGA AAGGCAATCT GAAAACCCAA ATCGAAACCC TCACCAAGCA  10500

GCCCGAGTAT GCTTATTTGA AACAACTTCA AGTTGCGAAA AACATCAACT GGAATCAGGT  10560

GCAGCTTGCT TACGATAAAT GGGACTACAA ACAGGAGGGC ATGACACCCG CAGCAGCAGC  10620

TGTCGTCGTT ATCGTCGTAA CCGTATTGAC CTACGGTGCA CTGTCCGCCC CGGCAGCCGC  10680

CGGAACGGCG GGCGCGGCAG GCGCAGGAGC GGGAGGAGCC GCAGCAGGAA CGGCAGCCGG  10740

AACTGGAGTA GCAGCAGGAA CGGCAGCCAC AACCGGAGTA GCAGCAGGCA CATCAGCTGC  10800

AGCTATCACC ACAGCCGCAG GCAAAGCCGC ACTGGCCAGT CTCGCCAGCC AAGCCGCAGT  10860

TTCCCTCATC AACAACAAAG GAGACATAAA CCATACCCTG AAAGAACTGG GCAAAAGCAG  10920

CACCGTCAGA CAGGCCGCCA CCGCCGCCGT AACCGCAGGC GTACTGCAGG GCATAAGCGG  10980

GCTGAACACC CAAGCAGCCG AAGCCGTCAG CAAACATTTT CACAGTCCCG CAGCAGGCAA  11040

ACTGACCGCT AACCTGATCA ACAGCACCGC TGCCGCAAGT GTCCATACCG CCATCAACGG  11100

CGGCAGCCTG AAAGACAACT TGGGCGATGC CGCACTGGGT GCGATAGTCA GTACCGTACA  11160

CGGAGAAGTA GCGAGCAAAA TCAAATTTAA TCTCAGCGAA GACTACATTG CCCACAAGAT  11220

AGCCCATGCC GTAGCAGGCT GTGCATCGGC GGTAGCAAAT AAAGGCAAAT GTCGGGACGG  11280

CGCAATCGGC GCGGCAGTCG GCGAGATGGT GGGAGAAACC CTGTTGGACG GACGCGATGT  11340

AGGCAAACTG TCACCCCAAG AACGCCAAAA AGTCATAGCC TACTCGCAGA TTATCGCAGG  11400

CAGCGCAGTG GCATTGGTTA AAGGGGATGT GAATACGGCG GTGAATGCGG CTACTGTGGC  11460

AGTGGAGAAT AATAGTCTTT TAGCTCGCAG GAGGGTAAAT ATACGTTGGA CTCCGCGACA  11520

AGAATTGGAA CATGAATATG CCATTCTTGA AATCCAGGCC ATTACCAATC AAATCCGAAG  11580

GCTGGATCCG AAATTTAACG GGATTGCTAT TCTGAGGACT CCTGGAGAGC CGTGGACAAG  11640

ACATGATGTA CAAACATACA GGCAATATTA TAATCAATTA AGGGAATCCA GAGGCTTTGC  11700

TGTTGAACCA ATTTATAGAA TCAGGATAAA CAACGGCAAT GAATTTAACC GTATCATGTC  11760

ATCAAAATAC CCTTATAATG AGCTTTATGT AGCCAATCCT AAATCGGCGA CGGGGTATTT  11820

TAGGGTAGAT TCGTATGATC CTGCGACAAG GGAAATTATT TCAAGAAAAT TTACCCAATT  11880

TTCTCAAATC CAAGAAAGTA CGGGGATTGG TTATATCAAG GAGGCTGTTA GAAAATATAG  11940

CCCTGGTACT GTCATTTCCA ATGTTCCAAG TACACCTACT ACGATAAGAG GAAGAAAGCT  12000

TGAAGGAAAA CTTATTTTAG AAGTTCCTGC TCAGGTCAAT CCAATTCCAC AATCTGTATT  12060

AAGGGCGGCA CAAGAAGAAA ATGTTATCAT TAGAGATACA ACAGGAAGGA TTTACAAATG  12120

AAGAAAGATA TTTTTTATTG TGAGCAGTGG TCTTATGGTT ATAAGAGACT TCATAAGCCT  12180

TTTTCTGAGA AACAAGCTGA GGAAAAACAT CTTAAAGGGG AGTTATATAC TGCCGTAATA  12240

GGTTCGGCGA CACAACCTGA ATATGTAATT ACCTTGCGAG AGGAAGTAGG TTTTTTTTCG  12300
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GTAAATTTTT TCGATAAATT TGGAAGGGAT TATTTAACCC ATCAATTTCA AAAATATTCC 12360

AATTCGAATT ATTATTTTCT TTCTATGGCT GTATGGAGAG ATTATATAAC TTTGGAATCT 12420

CATGACTTAG CAGAAGGATA TACTTATTTC TTCAATGAAA ATACGGATGA TTGCTATGTT 12480

TTGAAACAAG ATTTTATTAA TAATGAGCGA TATGAAAAAA CAGAATTATA TTCCCAAAAA 12540

GATAAGGTAA TTCTATTTCC AAAGTTTGGT GAATATGATT TGGTGTTAAA TCCGGACATT 12600

ATTTAATTAA GTTTTAAGGC CGTCTGAAAA AAATTTCAAA CGGCTTTTAT TATTGGGTTT 12660

GGAATCTGAG GATAAAGCTG ATAAAAACCA GGAAATTATC AGATTGCTAT ATACGTATTG 12720

TTGTACAGAC TAAAGGCAGC AATCAAATCA CTATTGCTTA CCCACAAAAA TAAATTGATT 12780

ATATGGAATA ATCATGAATA AGAGAATGAA AATGTGTCCT GCTTGTCAAC AAGGCTATCT 12840

CTACCATTCG AAACCTAAAT ATCTTCATGA TGAAATTATT CTGTGTGATG AATGCGATGC 12900

AGTATGGCTC AAAGGTATGA ATATATTTTA TGGAGAATAT GAAAAAGATT TTTATTCTTA 12960

TGTTCCTTTC ATGGAATCCC AAGGTATAAC GAGTGAATGT ATTTGGGAAG GAGATTTGTT 13020

TGATCATCCA TATTATGAAG ATGAAAACTC AAATGATATG GATTGATGGA AATTTTAAGC 13080

CTGCGTAGGT ACGATTAGCC ATCAAACGGC GTAATCATAC GCAAGATTAT CAACAGAGAG 13140

GGCTGGCAGC GATATACCAC CCACAAGATT GCCCATGCCA TAGCGGGCTG TGCGGCAGCG 13200

GCGGCGAATA AGGGCAAGTG TCAGGATGGT GCGATAGGCG CTGCAGTCGG TGAGATTGTT 13260

GGTGAGGCTT TGGTTAAGAA TACTGATTTC AGTCGTATGA GTGCGACCGA AATCGAAAAA 13320

GCTAAAGCGA AGATTACTGC CTATTCAAAA CTGGTTGCCG GCACTGCGTC TGCCGTTGTA 13380

GGCGGGGATG TGAATACAGC GGCGAATGCG GCACAGATAG CGGTGGAGAA TAATACTTTG 13440

TATCCTAGAT GCGTTGGTGC AAAGTGTGAT GAATTTCAAA AGGAACAACA AAAATGGATA 13500

CGTGAAAATC CTGAAGAATA TCGAGAAGTT TTGCTTTTTC AGACAGGATT TATTCCAATT 13560

ATCGGTGATA TACAGAGTTT TGTACAAGCA CAGACCGCTG CCGATCACCT GTTTGCTTTG 13620

CTGGGTGTGG TTCCGGGTAT CGGTGAATCG ATACAGGCCT ATAAAGTAGC GAAAGCGGCA 13680

AAAAATTTAC AAGGCATGAA AAAAGCCTTG GACAAGGCAG CAACCGTTGC CACTGCACAG 13740

GGCTATGTCA GCAAAACCAA AATCAAAATC GGTCAAACTG AATTAAGGGT TACTGCAGCA 13800

ACTGACAAAC AATTGCTGAA AGCTATTGGC GAAGGAAGGG ACACGACAGG TAAAATGACC 13860

GAGCAGTTAT TTGACTCTTT AGCTAAACAA AATGGCTTCA GAGTGCTTTC GGGCGGCAAA 13920

TACGGCGGAA ATAACGGTTT TGATCATGTA TGGCAGGCTG CCGATGGTAG TGTCGTTTTG 13980

ATTGTAGAAA GTAAGCAGAT TAGGAACGGT ACGGTACAGC TGAATCCGAA TGGTGCGGGT 14040

GGATATACGC AAATGAGTGA GGATTGGATT AGACAAGTTT TAGATCAATT ACCCGATGGT 14100

AGTCCCGCTA AAGCTGCTGT CTTCAAAGCA AATAAGAACG GCACATTAAA AACAGCAATA 14160

GCAGGCGTTG ATCGTCAAAC AGGTAAGGCC GTTATTCTTC CTGTCAAAGT TCCTTCTAAA 14220

ACCAATATAA GGAGATAACA ATGGGGCACA ATATGATGAC CACCCAAAAA TGGTATGAGC 14280

ATATTACTAA TGTAATCATA GGCAATACTG CTAATTTCAA TAGCGGTTGC CTTGACTCTA 14340

TAGATTATGT AGATGAAAGA AAAGGCGTTC CGCTTGCAGC TATGCAACAT ATTTTCATGG 14400

ACGTTAGAGC TGCAGCTTCC CATGCCTATC TATTTGAACA TGATCTTAAG AAATTCAAGC 14460

AATATGCTTA TGTTGCAGGA AAGCTGGGGG TTTTGCTGAG TGTAAATTCT ACAGACCCTG 14520

AACCCTTCTT CTTTCCCTGT GACATGCTCA ACATTCAAAA TCCGATGTTT CTGATGCTGA 14580

TGAGCGACAG CCCACAGCTG CGTGAGTTTC TGGTGCGCAA TATCGACAAC ATCGCCAACG 14640

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ATACAGAAGC CTTTATAAAC CGCTACGACC TCAACCGGCA TATGATTTAC AATACTCTGC  14700

TGATGGTGGA GGGTAAGCAG CTTGATCGGT TGAAACAACG TAGCGAGAAA GTCTTGGCGC  14760

ATCCCACCCC TAGCAAATGG CTGCAAAAGC GGTTGTACGA TTACCGCTTC TTCCTCGCTT  14820

TCGCCGAACA GGATGCCGAG GCAATGAAAG CCGCCTTAGA GCCGCTTTTC GATAAAAAAA  14880

CCGCGCGTAT GGCTGCCAAA GAAACATTGT CCTATTTCGA TTTCTACCTG CAGCCGCAAA  14940

TCGTTACCTA CGCCAAAATC GCATCCATGC ACGGTTTCGA TTTGGGCATA GATCAAGAAA  15000

TCTCACCGAG GGATTTGATT GTTTACGATC CGCTGCCGGC AGACGAATAT CAAGACATCT  15060

TCGATTTTAT GAAACAGTAT GACTTGTCTT ACCCGTATGA ATATCTGCAG GATTGGATAG  15120

ATTACTATAC GTTCAAAACC GATAAGCTGG TATTTGGTAA CGCGAAGCGA GAGTGAGCCG  15180

TAAAACTCTG AGCTCCTGTT TTATAGATTA CAACTTTAGG CCGTCTTAAA GCTGAAAGAT  15240

TTTCGAAAGC TATAAATTGA AGCCCTTCCA CAGTACATAG ATCTGTGTTG TGGCGGGGCT  15300

TTACCACGCT GATTGCCGGA GAAGAACTCA ACCTGCTGGC AAAACAAGGC ATGAGATCTT  15360

TGCAATAACA TGAGTTGAGA CCTTTGCAAA AAAGCCCTTC CCCGACATCC GAAACCCAAA  15420

CACAGGATTT CGGCTGTTTT CGTACCAAAT ACCTCCTAAT TTTACCCAAA TACCCCCTTA  15480

ATCCTCCTCG GACACCCGAT AATCAGGCAT CCGGGCTGCC TTTTAGGCGG CAGCGGGCGC  15540

ATTTAGCCTG TTGGCCGCTT TCAACAGGTT CAAACACATC GCCTTCAGGT GGCTTTGCGC  15600

ACTCACTTTG TCATTTCCAA                                              15620
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(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 580 acides amin,s
(B) TYPE: acide amin,
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION:1..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```
Met Lys Phe Phe Pro Ala Pro Cys Leu Leu Val Ile Leu Ala Val Ile
1               5                   10                  15

Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg
            20                  25                  30

Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala
        35                  40                  45

Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser
    50                  55                  60

Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp
65                  70                  75                  80

Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu
                85                  90                  95

Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg
            100                 105                 110

Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr
        115                 120                 125

Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys
    130                 135                 140

Leu Arg Val Ser Ala Gly Glu Ile Gly Asp Ile Arg Tyr Glu Glu Lys
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145                 150                 155                 160

Arg Asp Gly Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys
                165                 170                 175

Phe Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln
            180                 185                 190

Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln
        195                 200                 205

Ile Ile Pro Ser Glu Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp
    210                 215                 220

Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly
225                 230                 235                 240

Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Phe Asp
                245                 250                 255

Asn Pro Leu Gly Leu Ser Asp Leu Phe Tyr Val Ser Tyr Gly Arg Gly
            260                 265                 270

Leu Val His Lys Thr Asp Leu Thr Asp Ala Thr Gly Thr Glu Thr Glu
        275                 280                 285

Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys Lys
    290                 295                 300

Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr
305                 310                 315                 320

Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser
                325                 330                 335

Ser Leu Ala Ala Glu Arg Met Leu Trp Arg Asn Arg Phe His Lys Thr
            340                 345                 350

Ser Val Gly Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp
        355                 360                 365

Asp Ala Glu Ile Glu Val Gln Arg Arg Arg Ser Ala Gly Trp Glu Ala
    370                 375                 380

Glu Leu Arg His Arg Ala Tyr Leu Asn Arg Trp Gln Leu Asp Gly Lys
385                 390                 395                 400

Leu Ser Tyr Lys Arg Gly Thr Gly Met Arg Gln Ser Met Pro Ala Pro
                405                 410                 415

Glu Glu Asn Gly Gly Gly Thr Ile Pro Gly Thr Ser Arg Met Lys Ile
            420                 425                 430

Ile Thr Ala Gly Leu Asp Ala Ala Ala Pro Phe Met Leu Gly Lys Gln
        435                 440                 445

Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro
    450                 455                 460

Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg
465                 470                 475                 480

Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp
                485                 490                 495

Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu
            500                 505                 510

Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser
        515                 520                 525

Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys
    530                 535                 540

Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His
545                 550                 555                 560

Lys Pro Lys Gly Phe Gln Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu
                565                 570                 575
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Asn Tyr Ser Phe
580

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1981 acides amin,s
(B) TYPE: acide amin,
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION:1..1981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Asn Lys Gly Leu His Arg Ile Ile Phe Ser Lys Lys His Ser Thr
1 5 10 15

Met Val Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln
20 25 30

Ala Gly Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Leu Cys
35 40 45

Gly Lys Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser
50 55 60

Leu Ser Met Val Leu Pro Ala His Ala Gln Ile Thr Thr Asp Lys Ser
65 70 75 80

Ala Pro Lys Asn Gln Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala
85 90 95

Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn
100 105 110

Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn
115 120 125

Asp Arg Asn Asn Asn Pro Phe Leu Val Lys Gly Ser Ala Gln Leu Ile
130 135 140

Leu Asn Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr
145 150 155 160

Val Gly Gly Gln Lys Ala Asp Val Ile Ile Ala Asn Pro Asn Gly Ile
165 170 175

Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr
180 185 190

Ile Gly Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp
195 200 205

Val Arg Gln Gly Thr Leu Thr Val Gly Ala Ala Gly Trp Asn Asp Lys
210 215 220

Gly Gly Ala Asp Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln
225 230 235 240

Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys
245 250 255

Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr
260 265 270

Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala
275 280 285

Asp Ser Ile Thr Leu Ile Ala Asn Glu Lys Gly Val Gly Val Lys Asn
290 295 300

Ala Gly Thr Leu Glu Ala Ala Lys Gln Leu Ile Val Thr Ser Ser Gly

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305                 310                 315                 320

Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu
                325                 330                 335

Ala Ser Pro Thr Tyr Leu Ser Ile Glu Thr Thr Glu Lys Gly Ala Ala
            340                 345                 350

Gly Thr Phe Ile Ser Asn Gly Gly Arg Ile Glu Ser Lys Gly Leu Leu
        355                 360                 365

Val Ile Glu Thr Gly Glu Asp Ile Ser Leu Arg Asn Gly Ala Val Val
    370                 375                 380

Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala Gly His
385                 390                 395                 400

Asn Leu Val Ile Glu Ser Lys Thr Asn Val Asn Asn Ala Lys Gly Ser
                405                 410                 415

Ala Asn Leu Ser Ala Gly Gly Arg Thr Thr Ile Asn Asp Ala Thr Ile
            420                 425                 430

Gln Ala Gly Ser Ser Val Tyr Ser Ser Thr Lys Gly Asp Thr Glu Leu
        435                 440                 445

Gly Glu Asn Thr Arg Ile Ile Ala Glu Asn Val Thr Val Leu Ser Asn
    450                 455                 460

Gly Ser Ile Gly Ser Ala Ala Val Ile Glu Ala Lys Asp Thr Ala His
465                 470                 475                 480

Ile Glu Ser Gly Lys Pro Leu Ser Leu Glu Thr Ser Thr Val Ala Ser
                485                 490                 495

Asn Ile Arg Leu Asn Asn Gly Asn Ile Lys Gly Gly Lys Gln Leu Ala
            500                 505                 510

Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu Asn Thr
        515                 520                 525

Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val
    530                 535                 540

Asp Lys Asp Leu Ser Ala Ala Ser Ile His Leu Lys Ser Asp Asn Ala
545                 550                 555                 560

Ala His Ile Thr Gly Thr Ser Lys Thr Leu Thr Ala Ser Lys Asp Met
                565                 570                 575

Gly Val Glu Ala Gly Leu Leu Asn Val Thr Asn Thr Asn Leu Arg Thr
            580                 585                 590

Asn Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile Gln Leu
        595                 600                 605

Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr Ala Leu
    610                 615                 620

Gln Gly Asn Ile Val Ser Asp Gly Leu His Ala Val Ser Ala Asp Gly
625                 630                 635                 640

His Val Ser Leu Leu Ala Asn Gly Asn Ala Asp Phe Thr Gly His Asn
                645                 650                 655

Thr Leu Thr Ala Lys Ala Asp Val Asn Ala Gly Ser Val Gly Lys Gly
            660                 665                 670

Arg Leu Lys Ala Asp Asn Thr Asn Ile Thr Ser Ser Ser Gly Asp Ile
        675                 680                 685

Thr Leu Val Ala Gly Asn Gly Ile Gln Leu Gly Asp Gly Lys Gln Arg
    690                 695                 700

Asn Ser Ile Asn Gly Lys His Ile Ser Ile Lys Asn Asn Gly Gly Asn
705                 710                 715                 720

Ala Asp Leu Lys Asn Leu Asn Val His Ala Lys Ser Gly Ala Leu Asn
                725                 730                 735
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Ile His Ser Asp Arg Ala Leu Ser Ile Glu Asn Thr Lys Leu Glu Ser
            740                 745                 750

Thr His Asn Thr His Leu Asn Ala Gln His Glu Arg Val Thr Leu Asn
        755                 760                 765

Gln Val Asp Ala Tyr Ala His Arg His Leu Ser Ile Thr Gly Ser Gln
    770                 775                 780

Ile Trp Gln Asn Asp Lys Leu Pro Ser Ala Asn Lys Leu Val Ala Asn
785                 790                 795                 800

Gly Val Leu Ala Leu Asn Ala Arg Tyr Ser Gln Ile Ala Asp Asn Thr
                805                 810                 815

Thr Leu Arg Ala Gly Ala Ile Asn Leu Thr Ala Gly Thr Ala Leu Val
            820                 825                 830

Lys Arg Gly Asn Ile Asn Trp Ser Thr Val Ser Thr Lys Thr Leu Glu
        835                 840                 845

Asp Asn Ala Glu Leu Lys Pro Leu Ala Gly Arg Leu Asn Ile Glu Ala
    850                 855                 860

Gly Ser Gly Thr Leu Thr Ile Glu Pro Ala Asn Arg Ile Ser Ala His
865                 870                 875                 880

Thr Asp Leu Ser Ile Lys Thr Gly Gly Lys Leu Leu Leu Ser Ala Lys
                885                 890                 895

Gly Gly Asn Ala Gly Ala Pro Ser Ala Gln Val Ser Ser Leu Glu Ala
            900                 905                 910

Lys Gly Asn Ile Arg Leu Val Thr Gly Glu Thr Asp Leu Arg Gly Ser
        915                 920                 925

Lys Ile Thr Ala Gly Lys Asn Leu Val Val Ala Thr Thr Lys Gly Lys
    930                 935                 940

Leu Asn Ile Glu Ala Val Asn Asn Ser Phe Ser Asn Tyr Phe Pro Thr
945                 950                 955                 960

Gln Lys Ala Ala Glu Leu Asn Gln Lys Ser Lys Glu Leu Glu Gln Gln
                965                 970                 975

Ile Ala Gln Leu Lys Lys Ser Ser Pro Lys Ser Lys Leu Ile Pro Thr
            980                 985                 990

Leu Gln Glu Glu Arg Asp Arg Leu Ala Phe Tyr Ile Gln Ala Ile Asn
        995                 1000                1005

Lys Glu Val Lys Gly Lys Lys Pro Lys Gly Lys Glu Tyr Leu Gln Ala
    1010                1015                1020

Lys Leu Ser Ala Gln Asn Ile Asp Leu Ile Ser Ala Gln Gly Ile Glu
1025                1030                1035                1040

Ile Ser Gly Ser Asp Ile Thr Ala Ser Lys Lys Leu Asn Leu His Ala
                1045                1050                1055

Ala Gly Val Leu Pro Lys Ala Ala Asp Ser Glu Ala Ala Ala Ile Leu
            1060                1065                1070

Ile Asp Gly Ile Thr Asp Gln Tyr Glu Ile Gly Lys Pro Thr Tyr Lys
        1075                1080                1085

Ser His Tyr Asp Lys Ala Ala Leu Asn Lys Pro Ser Arg Leu Thr Gly
    1090                1095                1100

Arg Thr Gly Val Ser Ile His Ala Ala Ala Ala Leu Asp Asp Ala Arg
1105                1110                1115                1120

Ile Ile Ile Gly Ala Ser Glu Ile Lys Ala Pro Ser Gly Ser Ile Asp
                1125                1130                1135

Ile Lys Ala His Ser Asp Ile Val Leu Glu Ala Gly Gln Asn Asp Ala
            1140                1145                1150
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Tyr Thr Phe Leu Lys Thr Lys Gly Lys Ser Gly Lys Ile Ile Arg Lys
        1155                1160                1165

Thr Lys Phe Thr Ser Thr Arg Asp His Leu Ile Met Pro Ala Pro Val
    1170                1175                1180

Glu Leu Thr Ala Asn Gly Ile Thr Leu Gln Ala Gly Gly Asn Ile Glu
1185                1190                1195                1200

Ala Asn Thr Thr Arg Phe Asn Ala Pro Ala Gly Lys Val Thr Leu Val
                1205                1210                1215

Ala Gly Glu Glu Leu Gln Leu Leu Ala Glu Glu Gly Ile His Lys His
            1220                1225                1230

Glu Leu Asp Val Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly
        1235                1240                1245

Lys Ser Asn Tyr Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val
    1250                1255                1260

Arg Val Val Ala Gln Thr Ala Ala Thr Arg Ser Gly Trp Asp Thr Val
1265                1270                1275                1280

Leu Glu Gly Thr Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln
                1285                1290                1295

Ala Gly Val Gly Glu Lys Ala Arg Val Asp Ala Lys Ile Ile Leu Lys
            1300                1305                1310

Gly Ile Val Asn Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser
        1315                1320                1325

Thr Val Trp Gln Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu
    1330                1335                1340

Lys Leu Pro Ser Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro
1345                1350                1355                1360

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile
                1365                1370                1375

Glu Lys Leu Ser Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln
            1380                1385                1390

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg
        1395                1400                1405

Trp Asp Tyr Lys Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile
    1410                1415                1420

Ala Leu Ala Val Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val
1425                1430                1435                1440

Leu Gly Leu Asn Gly Ala Ala Ala Ala Ala Thr Asp Ala Ala Phe Ala
                1445                1450                1455

Ser Leu Ala Ser Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asp
            1460                1465                1470

Val Gly Lys Thr Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn
        1475                1480                1485

Leu Val Val Ala Ala Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala
    1490                1495                1500

Ser Ala Leu Asn Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr
1505                1510                1515                1520

Val Asn Leu Ala Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val
                1525                1530                1535

Asn Gly Gly Ser Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala
            1540                1545                1550

Leu Val Asn Thr Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu
        1555                1560                1565

Asp Gln His Tyr Ile Val His Lys Ile Ala His Ala Ile Ala Gly Cys
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    1570                1575                1580

Ala Ala Ala Ala Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly
1585                1590                1595                1600

Ala Ala Val Gly Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn
                1605                1610                1615

Pro Asp Thr Leu Thr Ala Lys Glu Arg Glu Gln Ile Leu Ala Tyr Ser
            1620                1625                1630

Lys Leu Val Ala Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn
        1635                1640                1645

Ala Ala Ala Asn Ala Ala Glu Val Ala Val Lys Asn Asn Gln Leu Ser
    1650                1655                1660

Asp Lys Glu Gly Arg Glu Phe Asp Asn Glu Met Thr Ala Cys Ala Lys
1665                1670                1675                1680

Gln Asn Asn Pro Gln Leu Cys Arg Lys Asn Thr Val Lys Lys Tyr Gln
                1685                1690                1695

Asn Val Ala Asp Lys Arg Leu Ala Ala Ser Ile Ala Ile Cys Thr Asp
            1700                1705                1710

Ile Ser Arg Ser Thr Glu Cys Arg Thr Ile Arg Lys Gln His Leu Ile
        1715                1720                1725

Asp Ser Arg Ser Leu His Ser Ser Trp Glu Ala Gly Leu Ile Gly Lys
    1730                1735                1740

Asp Asp Glu Trp Tyr Lys Leu Phe Ser Lys Ser Tyr Thr Gln Ala Asp
1745                1750                1755                1760

Leu Ala Leu Gln Ser Tyr His Leu Asn Thr Ala Ala Lys Ser Trp Leu
                1765                1770                1775

Gln Ser Gly Asn Thr Lys Pro Leu Ser Glu Trp Met Ser Asp Gln Gly
            1780                1785                1790

Tyr Thr Leu Ile Ser Gly Val Asn Pro Arg Phe Ile Pro Ile Pro Arg
        1795                1800                1805

Gly Phe Val Lys Gln Asn Thr Pro Ile Thr Asn Val Lys Tyr Pro Glu
    1810                1815                1820

Gly Ile Ser Phe Asp Thr Asn Leu Lys Arg His Leu Ala Asn Ala Asp
1825                1830                1835                1840

Gly Phe Ser Gln Glu Gln Gly Ile Lys Gly Ala His Asn Arg Thr Asn
                1845                1850                1855

Phe Met Ala Glu Leu Asn Ser Arg Gly Gly Arg Val Lys Ser Glu Thr
            1860                1865                1870

Gln Thr Asp Ile Glu Gly Ile Thr Arg Ile Lys Tyr Glu Ile Pro Thr
        1875                1880                1885

Leu Asp Arg Thr Gly Lys Pro Asp Gly Gly Phe Lys Glu Ile Ser Ser
    1890                1895                1900

Ile Lys Thr Val Tyr Asn Pro Lys Lys Phe Ser Asp Asp Lys Ile Leu
1905                1910                1915                1920

Gln Met Ala Gln Asn Ala Ala Ser Gln Gly Tyr Ser Lys Ala Ser Lys
                1925                1930                1935

Ile Ala Gln Asn Glu Arg Thr Lys Ser Ile Ser Glu Arg Lys Asn Val
            1940                1945                1950

Ile Gln Phe Ser Glu Thr Phe Asp Gly Ile Lys Phe Arg Ser Tyr Phe
        1955                1960                1965

Asp Val Asn Thr Gly Arg Ile Thr Asn Ile His Pro Glu
    1970                1975                1980
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(2) INFORMATION FOR SEQ ID NO: 39:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 acides amin,s
(B) TYPE: acide amin,
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION:1..143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```
Met Lys Asn Asn Ile Phe Leu Asn Leu Asn Lys Lys Ser Ile Asn Asn
1               5                  10                  15

Asn His Phe Val Ile Ser Ile Phe Phe Glu Thr Ile Tyr Gln Phe Glu
            20                  25                  30

Thr Lys Asp Thr Leu Leu Glu Cys Phe Lys Asn Ile Thr Thr Thr Gly
        35                  40                  45

His Phe Gly Val Ile Gly Ala Gln Tyr Glu Lys Ile Asp Ala Thr Arg
    50                  55                  60

Trp Ile Gly Asp Tyr Glu Glu Val Asn Gly Phe Glu Tyr Ile Asp Lys
65                  70                  75                  80

Ala Pro Ser Ile Tyr Phe Ser Val Gly Asp Asp Phe Asn Pro Glu Glu
                85                  90                  95

Leu Ile Ile Pro Ile Asn Leu Ala Tyr His Tyr Phe Asn Ile Ala Ile
            100                 105                 110

Ser Asp Phe Leu Ile Ala His Pro Glu Tyr Gln Lys Lys Cys Lys Glu
        115                 120                 125

Ile Gln Lys Thr Tyr Ser Gln Thr Asn Cys Ser Leu His Glu Thr
    130                 135                 140
```

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 acides amin,s
(B) TYPE: acide amin,
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION:1..833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```
Val Leu Lys Thr Pro Pro Thr Leu Ala Ala Glu Leu Ser Gly Lys Thr
1               5                  10                  15

Gly Val Ser Ile Ser Ala Pro Tyr Ala Asn Glu Asn Ser Arg Ile Leu
            20                  25                  30

Leu Ser Thr Thr Asp Ile Ser Ser Glu Asn Gly Lys Ile Lys Ile Gln
        35                  40                  45

Ser Tyr Gly Asp Gln Tyr Tyr Tyr Ala Arg Gln Ser Glu Leu Tyr Thr
    50                  55                  60

Phe Glu Arg Arg Ser Tyr Lys Thr Gly Lys Trp Tyr Asn Arg Lys His
65                  70                  75                  80

Ile Thr Glu Val Lys Glu His Lys Asn Ala Lys Pro Asp Ala Val Asn
                85                  90                  95

Leu Ser Ala Ser Gln Gly Ile Asp Ile Lys Ser Gly Gly Ser Ile Asp
            100                 105                 110
```

-continued

```
Ala Tyr Ala Thr Ala Phe Asp Ala Pro Lys Gly Ser Ile Asn Ile Glu
        115                 120                 125

Ala Gly Arg Lys Leu Thr Leu Tyr Ala Val Glu Glu Leu Asn Tyr Asp
    130                 135                 140

Lys Leu Asp Ser Gln Lys Arg Arg Arg Phe Leu Gly Ile Ser Tyr Ser
145                 150                 155                 160

Lys Ala His Asp Thr Thr Thr Gln Val Met Lys Thr Ala Leu Pro Ser
                165                 170                 175

Arg Val Val Ala Glu Ser Ala Asn Leu Gln Ser Gly Trp Asp Thr Lys
            180                 185                 190

Leu Gln Gly Thr Gln Phe Glu Thr Thr Leu Gly Gly Ala Thr Ile Arg
        195                 200                 205

Ala Gly Val Gly Glu Gln Ala Arg Ala Asp Ala Lys Ile Ile Leu Glu
    210                 215                 220

Gly Ile Lys Ser Ser Ile His Thr Glu Thr Val Ser Ser Ser Lys Ser
225                 230                 235                 240

Thr Leu Trp Gln Lys Gln Ala Gly Arg Gly Ser Asn Ile Glu Thr Leu
                245                 250                 255

Gln Leu Pro Ser Phe Thr Gly Pro Val Ala Pro Val Leu Ser Ala Pro
            260                 265                 270

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Gln Ile
        275                 280                 285

Glu Thr Leu Thr Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln
    290                 295                 300

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys
305                 310                 315                 320

Trp Asp Tyr Lys Gln Glu Gly Met Thr Pro Ala Ala Ala Ala Val Val
                325                 330                 335

Val Ile Val Val Thr Val Leu Thr Tyr Gly Ala Leu Ser Ala Pro Ala
            340                 345                 350

Ala Ala Gly Thr Ala Gly Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala
        355                 360                 365

Ala Gly Thr Ala Ala Gly Thr Gly Val Ala Ala Gly Thr Ala Ala Thr
    370                 375                 380

Thr Gly Val Ala Ala Gly Thr Ser Ala Ala Ala Ile Thr Thr Ala Ala
385                 390                 395                 400

Gly Lys Ala Ala Leu Ala Ser Leu Ala Ser Gln Ala Ala Val Ser Leu
                405                 410                 415

Ile Asn Asn Lys Gly Asp Ile Asn His Thr Leu Lys Glu Leu Gly Lys
            420                 425                 430

Ser Ser Thr Val Arg Gln Ala Ala Thr Ala Ala Val Thr Ala Gly Val
        435                 440                 445

Leu Gln Gly Ile Ser Gly Leu Asn Thr Gln Ala Ala Glu Ala Val Ser
    450                 455                 460

Lys His Phe His Ser Pro Ala Ala Gly Lys Leu Thr Ala Asn Leu Ile
465                 470                 475                 480

Asn Ser Thr Ala Ala Ala Ser Val His Thr Ala Ile Asn Gly Gly Ser
                485                 490                 495

Leu Lys Asp Asn Leu Gly Asp Ala Ala Leu Gly Ala Ile Val Ser Thr
            500                 505                 510

Val His Gly Glu Val Ala Ser Lys Ile Lys Phe Asn Leu Ser Glu Asp
        515                 520                 525
```

-continued

```
Tyr Ile Ala His Lys Ile Ala His Ala Val Ala Gly Cys Ala Ser Ala
    530                 535                 540

Val Ala Asn Lys Gly Lys Cys Arg Asp Gly Ala Ile Gly Ala Ala Val
545                 550                 555                 560

Gly Glu Met Val Gly Glu Thr Leu Leu Asp Gly Arg Asp Val Gly Lys
                565                 570                 575

Leu Ser Pro Gln Glu Arg Gln Lys Val Ile Ala Tyr Ser Gln Ile Ile
            580                 585                 590

Ala Gly Ser Ala Val Ala Leu Val Lys Gly Asp Val Asn Thr Ala Val
        595                 600                 605

Asn Ala Ala Thr Val Ala Val Glu Asn Asn Ser Leu Leu Ala Arg Arg
    610                 615                 620

Arg Val Asn Ile Arg Trp Thr Pro Arg Gln Glu Leu Glu His Glu Tyr
625                 630                 635                 640

Ala Ile Leu Glu Ile Gln Ala Ile Thr Asn Gln Ile Arg Arg Leu Asp
                645                 650                 655

Pro Lys Phe Asn Gly Ile Ala Ile Leu Arg Thr Pro Gly Glu Pro Trp
            660                 665                 670

Thr Arg His Asp Val Gln Thr Tyr Arg Gln Tyr Tyr Asn Gln Leu Arg
        675                 680                 685

Glu Ser Arg Gly Phe Ala Val Glu Pro Ile Tyr Arg Ile Arg Ile Asn
    690                 695                 700

Asn Gly Asn Glu Phe Asn Arg Ile Met Ser Ser Lys Tyr Pro Tyr Asn
705                 710                 715                 720

Glu Leu Tyr Val Ala Asn Pro Lys Ser Ala Thr Gly Tyr Phe Arg Val
                725                 730                 735

Asp Ser Tyr Asp Pro Ala Thr Arg Glu Ile Ile Ser Arg Lys Phe Thr
            740                 745                 750

Gln Phe Ser Gln Ile Gln Glu Ser Thr Gly Ile Gly Tyr Ile Lys Glu
        755                 760                 765

Ala Val Arg Lys Tyr Ser Pro Gly Thr Val Ile Ser Asn Val Pro Ser
    770                 775                 780

Thr Pro Thr Thr Ile Arg Gly Arg Lys Leu Glu Gly Lys Leu Ile Leu
785                 790                 795                 800

Glu Val Pro Ala Gln Val Asn Pro Ile Pro Gln Ser Val Leu Arg Ala
                805                 810                 815

Ala Gln Glu Glu Asn Val Ile Ile Arg Asp Thr Thr Gly Arg Ile Tyr
            820                 825                 830

Lys
```

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 664 acides amin,s
(B) TYPE: acide amin,
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```
Val leu Lys Thr Pro Pro Thr Leu Ala Ala Glu leu Ser Gly Lys Thr
  1  5 10 15

Gly Val Ser Ile Ser Ala Pro Tyr Ala Asn Glu Asn Ser Arg Ile Leu
 20 25 30

Leu Ser Thr Thr Asp Ile Ser Ser Glu Asn Gly Lys Ile Lys Ile Gln
 35 40 45
```

-continued

```
Ser Tyr Gly Asp Gln Tyr Tyr Tyr Ala Arg Gln Ser Glu Leu Tyr Thr
 50 55 60

Phe Glu Arg Arg Ser Tyr Lys Thr Gly Lys Trp Tyr Asn Arg Lys His
 65 70 75 80

Ile Thr Glu Val Lys Glu His Lys Asn Ala Lys pro Asp Ala Val Asn
 85 90 95

Leu Ser Ala Ser Gln Gly Ile Asp Ile Lys Ser Gly Gly Ser Ile Asp
100105110

Ala Tyr Ala Thr Ala Phe Asp Ala Pro Lys Gly Ser Ile Asn Ile Glu
115120125

Ala GlyArg Lys Leu Thr leu Tyr Ala Val Glu Glu Leu Asn Tyr Asp
130135    140

Lys leu Asp Ser Gln Lys Arg Arg Arg Phe Leu Gly Ile Ser Tyr Ser
145150155160


Lys Ala His Asp Thr Thr Thr Gln Val Met Lys Thr Ala Leu Pro Ser
                165                 170                 175

Arg Val Val Ala Glu Ser Ala Asn Leu Gln Ser Gly Trp Asp Thr Lys
            180                 185                 190

Leu Gln Gly Thr Gln Phe Glu Thr Thr Leu Gly Gly Ala Thr Ile Arg
        195                 200                 205

Ala Gly Val Gly Glu Gln Ala Arg Ala Asp Ala Lys Ile Ile Leu Glu
    210                 215                 220

Gly Ile Lys Ser Ser Ile His Thr Glu Thr Val Ser Ser Ser Lys Ser
225                 230                 235                 240

Thr Leu Trp Gln Lys Gln Ala Gly Arg Gly Ser Asn Ile Glu Thr Leu
                245                 250                 255

Gln Leu Pro Ser Phe Thr Gly Pro Val Ala Pro Val Leu Ser Ala Pro
            260                 265                 270

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Gln Ile
        275                 280                 285

Glu Thr Leu Thr Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln
    290                 295                 300

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys
305                 310                 315                 320

Trp Asp Tyr Lys Gln Glu Gly Met Thr Pro Ala Ala Ala Ala Val Val
                325                 330                 335

Val Ile Val Val Thr Val Leu Thr Tyr Gly Ala Leu Ser Ala Pro Ala
            340                 345                 350

Ala Ala Gly Thr Ala Gly Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala
        355                 360                 365

Ala Gly Thr Ala Ala Gly Thr Gly Val Ala Ala Gly Thr Ala Ala Thr
    370                 375                 380

Thr Gly Val Ala Ala Gly Thr Ser Ala Ala Ala Ile Thr Thr Ala Ala
385                 390                 395                 400

Gly Lys Ala Ala Leu Ala Ser Leu Ala Ser Gln Ala Ala Val Ser Leu
                405                 410                 415

Ile Asn Asn Lys Gly Asp Ile Asn His Thr Leu Lys Glu Leu Gly Lys
            420                 425                 430

Ser Ser Thr Val Arg Gln Ala Ala Thr Ala Ala Val Thr Ala Gly Val
        435                 440                 445

Leu Gln Gly Ile Ser Gly Leu Asn Thr Gln Ala Ala Glu Ala Val Ser
    450                 455                 460
```

-continued

```
Lys His Phe His Ser Pro Ala Ala Gly Lys Leu Thr Ala Asn Leu Ile
465                 470                 475                 480

Asn Ser Thr Ala Ala Ala Ser Val His Thr Ala Ile Asn Gly Gly Ser
                485                 490                 495

Leu Lys Asp Asn Leu Gly Asp Ala Ala Leu Gly Ala Ile Val Ser Thr
            500                 505                 510

Val His Gly Glu Val Ala Ser Lys Ile Lys Phe Asn Leu Ser Glu Asp
        515                 520                 525

Tyr Ile Ala His Lys Ile Ala His Ala Val Ala Gly Cys Ala Ser Ala
    530                 535                 540

Val Ala Asn Lys Gly Lys Cys Arg Asp Gly Ala Ile Gly Ala Ala Val
545                 550                 555                 560

Gly Glu Met Val Gly Glu Thr Leu Leu Asp Gly Arg Asp Val Gly Lys
                565                 570                 575

Leu Ser Pro Gln Glu Arg Gln Lys Val Ile Ala Tyr Ser Gln Ile Ile
            580                 585                 590

Ala Gly Ser Ala Val Ala Leu Val Lys Gly Asp Val Asn Thr Ala Val
        595                 600                 605

Asn Ala Ala Thr Val Ala Val Glu Asn Asn Ser Leu Leu Ala Arg Arg
    610                 615                 620

Arg Val Asn Ile Arg Trp Thr Pro Arg Gln Glu Leu Glu His Glu Tyr
625                 630                 635                 640

Ala Ile Leu Glu Ile Gln Ala Ile Thr Asn Gln Ile Arg Arg Leu Asp
                645                 650                 655

Pro Lys Phe Asn Gly Ile Ala Ile Leu Arg Thr Pro Gly Glu Pro Trp
            660                 665                 670

Thr Arg His Asp Val Gln Thr Tyr Arg Gln Tyr Tyr Asn Gln Leu Arg
        675                 680                 685

Glu Ser Arg Gly Phe Ala Val Glu Pro Ile Tyr Arg Ile Arg Ile Asn
    690                 695                 700

Asn Gly Asn Glu Phe Asn Arg Ile Met Ser Ser Lys Tyr Pro Tyr Asn
705                 710                 715                 720

Glu Leu Tyr Val Ala Asn Pro Lys Ser Ala Thr Gly Tyr Phe Arg Val
                725                 730                 735

Asp Ser Tyr Asp Pro Ala Thr Arg Glu Ile Ile Ser Arg Lys Phe Thr
            740                 745                 750

Gln Phe Ser Gln Ile Gln Glu Ser Thr Gly Ile Gly Tyr Ile Lys Glu
        755                 760                 765

Ala Val Arg Lys Tyr Ser Pro Gly Thr Val Ile Ser Asn Val Pro Ser
    770                 775                 780

Thr Pro Thr Thr Ile Arg Gly Arg Lys Leu Glu Gly Lys Leu Ile Leu
785                 790                 795                 800

Glu Val Pro Ala Gln Val Asn Pro Ile Pro Gln Ser Val Leu Arg Ala
                805                 810                 815

Ala Gln Glu Glu Asn Val Ile Ile Arg Asp Thr Thr Gly Arg Ile Tyr
            820                 825                 830

Lys
```

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 acides amin,s
(B) TYPE: acide amin,
(C) STRANDEDNESS: single

-continued

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION:1..162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```
Met Lys Lys Asp Ile Phe Tyr Cys Glu Gln Trp Ser Tyr Gly Tyr Lys
1               5                   10                  15

Arg Leu His Lys Pro Phe Ser Glu Lys Gln Ala Glu Glu Lys His Leu
            20                  25                  30

Lys Gly Glu Leu Tyr Thr Ala Val Ile Gly Ser Ala Thr Gln Pro Glu
        35                  40                  45

Tyr Val Ile Thr Leu Arg Glu Glu Val Gly Phe Phe Ser Val Asn Phe
    50                  55                  60

Phe Asp Lys Phe Gly Arg Asp Tyr Leu Thr His Gln Phe Gln Lys Tyr
65                  70                  75                  80

Ser Asn Ser Asn Tyr Tyr Phe Leu Ser Met Ala Val Trp Arg Asp Tyr
                85                  90                  95

Ile Thr Leu Glu Ser His Asp Leu Ala Glu Gly Tyr Thr Tyr Phe Phe
            100                 105                 110

Asn Glu Asn Thr Asp Asp Cys Tyr Val Leu Lys Gln Asp Phe Ile Asn
        115                 120                 125

Asn Glu Arg Tyr Glu Lys Thr Glu Leu Tyr Ser Gln Lys Asp Lys Val
    130                 135                 140

Ile Leu Phe Pro Lys Phe Gly Glu Tyr Asp Leu Val Leu Asn Pro Asp
145                 150                 155                 160

Ile Ile
```

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 acides amin,s
(B) TYPE: acide amin,
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION:1..90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```
Met Asn Lys Arg Met Lys Met Cys Pro Ala Cys Gln Gln Gly Tyr Leu
1               5                   10                  15

Tyr His Ser Lys Pro Lys Tyr Leu His Asp Glu Ile Ile Leu Cys Asp
            20                  25                  30

Glu Cys Asp Ala Val Trp Leu Lys Gly Met Asn Ile Phe Tyr Gly Glu
        35                  40                  45

Tyr Glu Lys Asp Phe Tyr Ser Tyr Val Pro Phe Met Glu Ser Gln Gly
    50                  55                  60

Ile Thr Ser Glu Cys Ile Trp Glu Gly Asp Leu Phe Asp His Pro Tyr
65                  70                  75                  80

Tyr Glu Asp Glu Asn Ser Asn Asp Met Asp
                85                  90
```

(2) INFORMATION FOR SEQ ID NO: 44:

-continued

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 acides amin,s
(B) TYPE: acide amin,
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION:1..313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```
Met Ser Ala Thr Glu Ile Glu Lys Ala Lys Ala Lys Ile Thr Ala Tyr
1               5                  10                  15

Ser Lys Leu Val Ala Gly Thr Ala Ser Ala Val Val Gly Gly Asp Val
            20                  25                  30

Asn Thr Ala Ala Asn Ala Ala Gln Ile Ala Val Glu Asn Asn Thr Leu
        35                  40                  45

Tyr Pro Arg Cys Val Gly Ala Lys Cys Asp Glu Phe Gln Lys Glu Gln
    50                  55                  60

Gln Lys Trp Ile Arg Glu Asn Pro Glu Glu Tyr Arg Glu Val Leu Leu
65                  70                  75                  80

Phe Gln Thr Gly Phe Ile Pro Ile Ile Gly Asp Ile Gln Ser Phe Val
                85                  90                  95

Gln Ala Gln Thr Ala Ala Asp His Leu Phe Ala Leu Leu Gly Val Val
            100                 105                 110

Pro Gly Ile Gly Glu Ser Ile Gln Ala Tyr Lys Val Ala Lys Ala Ala
        115                 120                 125

Lys Asn Leu Gln Gly Met Lys Lys Ala Leu Asp Lys Ala Ala Thr Val
    130                 135                 140

Ala Thr Ala Gln Gly Tyr Val Ser Lys Thr Lys Ile Lys Ile Gly Gln
145                 150                 155                 160

Thr Glu Leu Arg Val Thr Ala Ala Thr Asp Lys Gln Leu Leu Lys Ala
                165                 170                 175

Ile Gly Glu Gly Arg Asp Thr Thr Gly Lys Met Thr Glu Gln Leu Phe
            180                 185                 190

Asp Ser Leu Ala Lys Gln Asn Gly Phe Arg Val Leu Ser Gly Gly Lys
        195                 200                 205

Tyr Gly Gly Asn Asn Gly Phe Asp His Val Trp Gln Ala Ala Asp Gly
    210                 215                 220

Ser Val Val Leu Ile Val Glu Ser Lys Gln Ile Arg Asn Gly Thr Val
225                 230                 235                 240

Gln Leu Asn Pro Asn Gly Ala Gly Gly Tyr Thr Gln Met Ser Glu Asp
                245                 250                 255

Trp Ile Arg Gln Val Leu Asp Gln Leu Pro Asp Gly Ser Pro Ala Lys
            260                 265                 270

Ala Ala Val Phe Lys Ala Asn Lys Asn Gly Thr Leu Lys Thr Ala Ile
        275                 280                 285

Ala Gly Val Asp Arg Gln Thr Gly Lys Ala Val Ile Leu Pro Val Lys
    290                 295                 300

Val Pro Ser Lys Thr Asn Ile Arg Arg
305                 310
```

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

-continued

(A) LENGTH: 311 acides amin,s
(B) TYPE: acide amin,
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION:1..311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
Met Gly His Asn Met Met Thr Thr Gln Lys Trp Tyr Glu His Ile Thr
1               5                  10                  15

Asn Val Ile Ile Gly Asn Thr Ala Asn Phe Asn Ser Gly Cys Leu Asp
            20                  25                  30

Ser Ile Asp Tyr Val Asp Glu Arg Lys Gly Val Pro Leu Ala Ala Met
        35                  40                  45

Gln His Ile Phe Met Asp Val Arg Ala Ala Ala Ser His Ala Tyr Leu
    50                  55                  60

Phe Glu His Asp Leu Lys Lys Phe Lys Gln Tyr Ala Tyr Val Ala Gly
65                  70                  75                  80

Lys Leu Gly Val Leu Leu Ser Val Asn Ser Thr Asp Pro Glu Pro Phe
                85                  90                  95

Phe Phe Pro Cys Asp Met Leu Asn Ile Gln Asn Pro Met Phe Leu Met
            100                 105                 110

Leu Met Ser Asp Ser Pro Gln Leu Arg Glu Phe Leu Val Arg Asn Ile
        115                 120                 125

Asp Asn Ile Ala Asn Asp Thr Glu Ala Phe Ile Asn Arg Tyr Asp Leu
    130                 135                 140

Asn Arg His Met Ile Tyr Asn Thr Leu Leu Met Val Glu Gly Lys Gln
145                 150                 155                 160

Leu Asp Arg Leu Lys Gln Arg Ser Glu Lys Val Leu Ala His Pro Thr
                165                 170                 175

Pro Ser Lys Trp Leu Gln Lys Arg Leu Tyr Asp Tyr Arg Phe Phe Leu
            180                 185                 190

Ala Phe Ala Glu Gln Asp Ala Glu Ala Met Lys Ala Ala Leu Glu Pro
        195                 200                 205

Leu Phe Asp Lys Lys Thr Ala Arg Met Ala Ala Lys Glu Thr Leu Ser
    210                 215                 220

Tyr Phe Asp Phe Tyr Leu Gln Pro Gln Ile Val Thr Tyr Ala Lys Ile
225                 230                 235                 240

Ala Ser Met His Gly Phe Asp Leu Gly Ile Asp Gln Glu Ile Ser Pro
                245                 250                 255

Arg Asp Leu Ile Val Tyr Asp Pro Leu Pro Ala Asp Glu Tyr Gln Asp
            260                 265                 270

Ile Phe Asp Phe Met Lys Gln Tyr Asp Leu Ser Tyr Pro Tyr Glu Tyr
        275                 280                 285

Leu Gln Asp Trp Ile Asp Tyr Tyr Thr Phe Lys Thr Asp Lys Leu Val
    290                 295                 300

Phe Gly Asn Ala Lys Arg Glu
305                 310
```

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleotide

-continued

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCCACCGGTA CGGAAACTGA A 21

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CCTGAATTCA TGTCTATTCC ATTTTGAAGA 30

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CCGAGATCTT TAACCCTTTG GGCTTAAGCG A 31

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GGGAGATCTC CCGCTCGTGT TGTGCATTA 29

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

-continued

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

AAGAGATCTG CAGCCAAGGC TCTCGAAA 28

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GGGAGATCTC AGGCTGCCGC CGTTGA 26

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGGAGATCTC ACCCCAAGAA CGCCAAAA 28

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGGAGATCTG AACGTATAGT AATCTATCCA A 31

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

-continued

AGTGGCTCCT AG 12

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

AGCACTCTCC AGCCTCTCAC CGAG 24

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

AGTGGCTCTT AA 12

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

AGTGGCTGGC 10

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AGCACTCTCC AGCCTCTCAC CGAC 24

-continued

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GTACTTGCCT AG 12

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACCGACGTCG ACTATCCATG AACG 24

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GTACTTGCTT AA 12

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GTACTTGGGC 10

(2) INFORMATION FOR SEQ ID NO: 63:

-continued

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGACGTCG ACTATCCATG AACC 24

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

AATTCTCCCT CG 12

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGGCAACTGT GCTATCCGAG GGAG 24

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GATCAACTTT TCCCTGTTTG TCCCATTACC GGTTTGAATG AACCGATTGC GCGCCGCGCG 60

TGTTGTTGGA CATTACCTGC GATTCAGACG GTACGATTGA CCACTACATC GAGGAGAACG 120

GCAATCAGGG TACAATGCTA 140

(2) INFORMATION FOR SEQ ID NO: 67:

-continued

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GATCCGCGTA CTTGGTTTTT CATATTTTGC ATAGTCTTGT CGGTCGGGCA TCTTCCCCGA 60

CATCATCTAA ATTTGTCTTT ATTGGTTTTT ACGCCACTCA TTGCGGATAA ACAATATTCC 120

GCCTTGCCGT CGCGAATGTT CAAGCTAGCC TGCATCACCG TAATCAGGTT GCCCGTTACC 180

GAGCCTTCGA GA 192

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GATCCGGCTG CCCGACGCGC GCAAAATTGC CGCCGAGGAA AGCGCGCACA ACCACGACGG 60

CAAAACCAGC GTATGGCAAT ACAAACATCT CGTGTTCGGT ACGGCAGGCA TTTTCTGCTA 120

TGTCGGCGCG GAGGTGTCTA TCGGTTCGTT GATGGTCAAC GTATTGGGTT ATCTGAAAGG 180

GCTGGATC 188

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GATCCCCCAC TTTACCTCGG GCAGATTTTG CGCGTTCATT ACAATAGCGT ATTTATGCGT 60

TTGCGTTTGC GCTTGCCGCT GCCCCCCCCC CGCCGGTATG GGAAAACATC AATATGGCGG 120

TATAAAGCGC GGTATGGCGG AAAACCTGCC GTTTCCAAGT TTTATTCATC TTTTATTCCT 180

TGAGTTTGCC TTCACGGGAC GGGGCGGCGC GCGGAACGCG GGGTTCGGTA AACCGCCCGA 240

TTCCGCGCCC GCCGAATTGC TGATTGAAAA GCTTACTTCC CCATTTTAAC TTTGCACACT 300

GATC 304

(2) INFORMATION FOR SEQ ID NO: 70:

-continued

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GATCAGACCC ATTTTCAGCG CACCGTAAGC GCGGATTTTC TCGAATTTTT CCAAAGCTGC 60

GGCATCGTTG TTGATGTCGT CTTGCAACTC TTTGCCCGTG TAGCCCAAGT CGGCGGCATT 120

CAGGAAAACG GTCGGAATGC CCGCGTTGAT GAGCGTGGCT TTCAAACGGC CTATATTCGG 180

CACATCAATT TCATCGACCA AATTGCCGGT TGGGAACATA CTGCCTTCGC CGTCGGCTGG 240

ATC 243

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CGGCGGCGTA GTCCGCCGCG ACAGCGTTAC CATAAGCGGG ACAGACTACA CCCCTTTATC 60

TAACCCGCAA AGTTTGGATA CGGAATTAAA ATGGTTGCTT CAAGAAGCTC CCGAAATAGA 120

AAATCCTTTC GACCGCGCCG TTTATCTCCA TAATAATTTG GCGTATCTTC AATATTTTAA 180

AGATTGCAAT AAACGTACTG CCAGAAACTG CATGACCTTG TCGCTGATGC GCTCCG 236

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CGGTCAATCA CAAGAAAGTC AGCCGTCTGA TGGCGAAGAC GGGGCTGAAG GCAGTGATAT 60

GGCGGCGCAA ATACCGCTCG TTCAAAGGAG AAGTCGGCAA AATTGCGCCG AATATCCTGC 120

GACGCTGTTT CCATGCAGAA AAGCCGAATG AGAAATGGGT AACGGACGTT GCCGAGTTCA 180

ATGTAGGCGG AGAAAAGATA TACCTTTCTC CGATTATGGA TTTGTTTAAC GGGGAAATCG 240

TCAGTTACCG TATTCAGACC CGCCCGACTT TCGATTTGGC 280

(2) INFORMATION FOR SEQ ID NO: 73:

-continued

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CGGTGTTTTT CTTAACAATT CGCCGACTTC ATGGCGATAT TTAAGTGACA GTTGCTCCGC 60

CCACGCAGTT GCGCCGAACT CAGCACCACG ACATTATACT GATTATGCAC ATCGGCAAGA 120

TCAAACTGAC CTATCGTAGT ATCGCAGACT GT 152

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

-continued

CGGGAGGTTT TGTGCATCCT GATACCGATC GGTTGTTGTT GCTCAAAGGA CAGAAGGCCG 60

CTGATAAACG AGATTACCTG TTTGTCGCTA TTGACGATTT TTATACTCTG CCATTTTGCC 120

AGACAAAACC GCAGACAGTG CTGCCAAGTT TCTGACCGAA CATCTGGCCG ACCCCTGCTT 180

GTACCTGATT GAGTACGCTT ACTCTGACAA TGATAGGTAA TATAAAGAGC CGTCCAACAT 240

GCTTTCGGTG CAGTTTGTTA TGATAATGGG ATTGGTTGGA GGCTTGCCCG ATTTGCTTGT 300

CCGCAGACCA ACGGTAAGGC GGAGCGGGTT ATCCGTACCT TGATGGAGAT GTGGCATGAG 360

GAACAGTCGT TTGACAGACC G 381

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CGGAGCATAA AATCGTTATT AAAGATAATG GTATAGGAAC GAGCTTCGAT GAAATCAATG 60

ATTTTTATTT GAGAATCGGT CGGAACAGAA GGGAAGAAAA ACAAGCCTCC CCGTGCGGAA 120

GAATTCCAAC GGGTAAAAAA GGCCTTGGTA AATTGGCATT ATTCGGGCTT GGCAACAAAA 180

TTGAAATTTC TACTATCCAG GGAAACGAAA GGGTTACTTT TACTTTGGAT TATGCAGAGA 240

TTCGAAGAAG CAAGGGTATT TATCAACCG 269

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CGGATGAAAA CGGCATACGC GCCAAAGTAT TTACGAACAT CAAAGGCTTG AAGATACCGC 60

ACACCTACAT AGAAACGGAC GCGAAAAAGC TGCCGAAATC GACAGATGAG CAGCTTTCGG 120

CGCATGATAT GTACGAATGG ATAAAGAAGC CCGAAAATAT CGGGTCTATT GTCATTGTAG 180

ATGAAGCTCA AGACGTATGG CCG 203

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

-continued

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

CGGTTTCAGG TTGTCGCGAA GGCTCGGTAA CGGGCAACCT GATTACGGGT GATGCAGGCA 60

GCTTGAACAT TCGCGACGGC AAGGCGGAAT ATGTTTATCC GCAATGAGTG GCGTAAAAAC 120

CAATAAAGAC AAATTTAGAT GATGTCGGGG AAGATGCCCG ACCGACAAGA CTATGCAAAA 180

TATGAAAAAC CAAGTACGCG GATCAGGCAT GGATGCACGA TCCAATCCG 229

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG TTTGGAAATA 60

TTGTGTATCG GGGGGGGGTA TTTGCTGACG TAAAAAACTA TAAACGCCGC GCAAAATATG 120

GCTGACTATA TTATTGACTT TGATTTTGTC CTGCGCGGTG ATGGATAAAA TCGCCAGCGA 180

TAAAGAATTT GCGAGAACCT GATGCCG 207

(2) INFORMATION FOR SEQ ID NO: 81 :

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CGGCAACGAT TTGAGCTATC GCGGTTACGA CATTCTGGAT TTGGCACAAA AATGCGAGTT 60

TGAAGAAGTC GCCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC 120

TTATAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTTGGA 180

AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG 224

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

-continued

CGGGAACAGC CATTGCCCAC GCCCACGCCC CCCAAGAAAG ACGGAAACTA CTGCCTAAAT 60

TTTCGGCAAT CAAGTTGACG ATTAAAGGGT TGGGGGCAGT TGCAGTAATA AACATAGCCG 120

ACGAAATGGG ATTGGAATGA TAGTTGACCA AAGCCAAATA TTTACCCATC TTGCCTTCTG 180

TGCCTTTTGC GGGATTGGAG CCGTAACTGC CG 212

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGGGAATTCT GAGCAGAATG AAAGAAAGCA GGCTTGATAA TTTCATAAAG TTATTGGAAG 60

AAAAAGGATT TACCGTCCAT TTCGGTATTC ACAATACGGC TGATTACGGA ATTCCCCAAA 120

GCCGTAAAAG ATTTACGTTA ATTGCAAACA GAATAACCAA AGAAAAGCTG GAACCAGTCA 180

AGTATTCGGG CAAACGGCTT ACGGTAGCCG ATGTTTTGGG AATGGAAATG GCTTTCCCAA 240

CATTATTGCA GGACACCAAG ACGAAACGGA TTTTATGCAT AGCTGTGCGG GAATTATCTG 300

ATATCACTTG AACGATTGGC TTGATACCTA AAAACGGAGG AACCGTTGGC TTT 353

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AATTCCGTAT CCAAACTTTG CGGGTTAGAT AAAGGGGTGT AGTCTGTCCC GCTTATGGTA 60

ACGCTGTCGC GGCGGACTAC GCCCGGAGCC TTTTTCCAGT AAGTTTTCGG AAATCAGGCT 120

GTGGGTGGTT TTTAAGAAAT CCAACCAGTC AAACGGCTCG GGGCTGTCCA AACCGGACAC 180

AGGTGCCGGT AACTTTCCCT CAGGTTGATT AACATTACGG CATCCGAATA TAACTTCCCG 240

CCTGCGGTTT GCCCGAGTTT AAGCAATGCC TGCGTATCGT ATTGATTATA AAGTGTTTCC 300

TTCCAATT 308

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

-continued

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AATTCGTGTG CCGCGTCGAC AAACCGCTGA CGTAGCGGAT GTCTCATGCC ACGTTTCAAA 60

GCAGGTTGAT GGCGGTTAGC AACCCTCTGA TTTCACTGGG ATAT 104

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

AATTGCGTAG AGTGGGCTTC AGCCACGTTT TTTCTTTTTC GGTCGTTGAT TGGTGGGCTG 60

AACCACTTGT TTCGGAAATC CGTATCATG 89

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AATTTCCACC TATGCCCTAC GCAGCGATTA TCCGTGGTTT ACCCAAAGGG TGATTATGGC 60

AAAAGCGCGG GGTTGAGCGA CCGCCTTTTG TTGCCGGCGT TCAAACGGGT TTTGATAGGA 120

AATGCAGGCA CGAAGCCTCG GCTGATTGTG ATGCACCTGA TGGGTTCGCA CAGTGATTTT 180

TGCACACGTT TGGATAAGGA TGCGCGGCGG TTTCAGTATC AAACTGAAAA AATATCCTGC 240

TATGTTTCCA TCAATCGCGC AAACCGATAA ATT 273

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

AATTCTTCCG CACGGGGAGG CTTGTTTTTC TTCCCTTCTG TTCCGACCGA TTCTCAAATA 60

AAAATCATTG ATTTCATCGA AGTTCATTCC TATACCATTA TCTTTAATAA CGATTTTATG 120

CTCCGGTTTA TCGAATAACC TAACTTCCAC TTCCGTAGCA CATGCATCGT AGGCATTCGC 180

-continued

TATCAACTCG GCAATCGCAG GAACAGTGTG CGAATACAAT CTTTACACCC AAATGTTCGA 240

TTACGGTTGG CTCGAAACTC AATTTCAATT 270

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

AATTATGAAC ACACGCATCA TCGTTTCGGC TGCGTTCGTT GCGTTGGCAT TAGCAGGTTG 60

CGGCTCAATC AATAATGTAA CCGTTTCCGA CCAGAAACTT CAGGAACGTG CCGCGTTTGC 120

CTTGGGCGTC ACCAATGCCG TAAAAATCAG CAACCGCAGC AATGAAGGCA TACGCATCAA 180

CTTTACCGCA ACTGTGGGTA AGCGCGTGAC CAATGCTATG TTACCAGTGT AATCAGCACA 240

ATCGGCGTTA CCACTTCCGA TGCAATT 267

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

AATTTTTATT TGGTTCGTAG TCATTTTGTG CAACTGAACG ATATTCGTTT TCATCATTGC 60

TAACGTCTAG TGCCCATTGT GGCCCGTAAT AAGAGATTTC GTCTCCTTTT ACATGTTTGA 120

CGCTGACGGC ATACTGGGGA TCGATGACGG ATAATGTACG TCTGTTGACA TCTGCAACGC 180

TAAATCAATC ATCGGTATTG GATAATGCGT TGCCGATGTT TTGACTTGTA TGTT 234

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AATTCGGCCG GCTGTGTCAA ATAATGCGTT ACTTTGGCCG GGTCTTGTTC TTTGTAAGTG 60

GTGGTCTTTT TTTGCGCGTT ATCCCCATCT GTTTGAGTGC ATAGCAAATG GTGGCTGCCG 120

TACAATCAAA TGTTTGGCGT TCATGCAGAT AGGCATCATG GTGTTGCCCA ATATATTGAG 180

-continued

CCGGTTTTTG CCTATCCGAT TTGACGGCAT TTAGACCGGT AACTTGATGT TTTAAGCTGC 240

CTGTTTGTTT AAAGGCGAAT CCACAAGTAA AGCGTGTTTC TTGACAGGTT AAACG 295

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

AATTGTGTAT ATCAAGTAGG ATGGGCATTT ATGCCTGACC TACAAAACCA AAAACAACCT 60

ACCACCCTTA ATCAACTCCA CAAACCCTCT TCAGACAACC TCGTTTTTTG AAAAACAATC 120

TGTAAACAGA TAACTGCTGA AGAATACCGT TGCCGAGCCC CAAAACCCGT ACTGCAACTT 180

TTATTGTGAA CTTCCCATTA TGAGAAAATC CCTTTTCGTC CTCTTTCTGT ATTCGTCCCT 240

ACTTACTGCC AGCGAAATT 259

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

AATTGCACCA CGCGATGATG GGTACGCCTC TGTTGCCATT GCGACCGCCG CCGCCGTGCC 60

CGGTACGCTG GTCAACCTTG CCGCGGCGGA ACGGGTAAAG AAGTGCGCTT CGGGCATCCT 120

TCCGGTACAT TGCGCGTCGG TGCAGCGCCG AATGTCAGGA CGGACAATGG ACGGCCACCA 180

AAGCGGTTAT GAGCCGCAGC GCACGCGTGA TGATGGAAGG TTGGGTCAGG GTGCCGGAAG 240

ATTGTTTTTA AATTGGACGG CGAACCGGTC TATTCGTATT GGCGTTATAC CGCCGCAAAG 300

GCAGACCTTG AAACTGGTGC GTGCCGTGCA GGGCATGTAC GGCTATGTGT GCGTGGCGGG 360

CGGATTTGAT GTGCGGAAT 379

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

-continued

AATTTGTTGG GCAGATGGCC GTGAATCAGC AGGTGGGCGA CTTCTTCAAA CTCGCATTTT 60

TGTGCCAAAT CCAGAATGTC GTAACCGCGA TACGTCAAAT CGTTGCCGGT ACGCAACGGT 120

ACACAAAGCG GTATTACCGG CCGCAACGCC AGAAAGCGCA ACGGATTTTT AGGTTTGAGG 180

GTCGGGGTTT GAGTAGTTTC AGTCATGGTA TTTCTCCTTT GTGTTTTTAT GGGTTTCGGG 240

TTTTCAGACG ACCGATGCGG ATTTGTTGAA AGGCAGTCTG AAAGCGGTAA ATCATTTTTG 300

AAACAATT 308

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AATTCGGAGG AGCAGTACCG CCAAGCGTTG CTCGCCTATT CCGGCGGTGA TAAAACAGAC 60

GAGGGTATCC GCCTGATGCA ACAGAGCGAT TACGGCAACT TGTCCTACCA CATCCGTAAT 120

AAAAACATGC TTTTCATTTT TTCGGCAAGC AATGACGCAC AAGCTCAGCC CAACACAACT 180

GACCCTATTG CCATTTTATG AAAAAGACGC TCAAAAAGGC ATTATCACAG TTGCAGGCGT 240

AGACCGCAGT GGAGAAAAGT TCAATGGCTC CAACCATTGC GGAATT 286

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AATTTGGATA CGTTGGAAAA GGGATATTTG ATTGGGAATG GGATGAAGAT AAGCGTAGAT 60

GAGTTGGGGA AAAAAGTGTT AGAACATATC GGTAAGAATG AACCGTTATT GTTGAAAAAT 120

CTACTGGTTA ACTTCAATCA GGGAAAACAT GAAGAAGTTA GGAAGTTGAT TTATCAGTTG 180

ATAGAGTTAG ATTTTCTGGA ACTTTTGTGA GGGATTCTAT GAAAAACTGG AAGCAATT 238

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

-continued

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AATTCGGCAC GCAGGTTTTC TAAAAAAAGG CCGTTGATGA CTTTGTCGAT ATTGGCGGCT 60

TCGGTGTAGT GCGCGCCCGC TTCGGCCGCT CTTGCGCGTC CATGACGGAT TGGAAGAGCG 120

TGCCGAAGAT TTCTGGACTG ATGTTGCGCC AGTCGAAATT GCCGACACGG GAGGAATACC 180

TGCCAACAAG AGTGCAGGCA GCGTAATCAA ACCACCCCCA CCCGCAATCG CATCGATAAA 240

TCCGGCAATC ATCGCAACCA AACCCAAAGC GAGTATTATG TATAAATCTT CCATGTTTCT 300

TAATCCTGTT AACTTGCACC AA 322

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

AATTTGTCGG CAATCTTCCC GGGTCGCTTT ATTTTGTGCA GGCATTATTT TTCATTTTTG 60

GCTTGACAGT TTGGAGATAT TGTGTATCGG GGGGGGGTAT TTGCTGACGT AAAAAACTAT 120

AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC CTGCGCGGTG 180

ATGGATAAAA TCGCCAGCGA TAAAGATTTG CGAGAACCTG ATGCCGGCCT GTTGTTGAAT 240

ATTTTCGACC TGTAATTACG ATTTGGCTTC CGCGCCGGCA CAATATGCCG CCAAGCGGCG 300

CCCACATTTT GGAAGC 316

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

AATTCGGACA GTATGAATAC AGCGGATTAA TACAAGGTAA GTTCATTACA ACGGAAAAAC 60

CTTTAAAGAA TAATATGAAA GGTATTACCT TGTTTGCCAA CGGGAATGGT AAATATGCCC 120

GAGTTTTTCA CTGAATAGCG AATCCAGCCA TTTCTATTCA TATTTGACTG GATGGCTGAA 180

TGTGGACTTT ATAGATAATG ACGATGAAGA TTTAATT 217

What is claimed is:

1. An isolated DNA which is specific to *Neisseria meningitidis* (Nm) and *Neisseria gonorrheae* (Ng), and hybridizes on a Southern blot to SEQ ID NO:95 and does not hybridize on a Southern blot to a DNA sequence of *Neisseria lactamica* (Nl) strain Nl8064, under the following hybridization conditions: 18 h at 65° C., with a solution comprising 0.5 M $NaPO_4$ pH 7.2, 0.001 M EDTA-Na, 1% bovine serum albumin and 7% sodium dodocylsulphate, followed by at least two washes in a solution comprising 40 mM Na PO_4 pH 7.2, 1 mM EDTA, and 1% SDST, the final wash being conducted at 85° C. for 5 minutes, or the complement of said isolated DNA which is specific to *Neisseria meningitidis* (Nm) and *Neisseria gonorrheae* (Ng),

provided that said DNA or the complement of said isolated DNA is not pilC, or a gene involved in the

biosynthesis of any one of the polysaccharide capsule, IgA proteases, pilin, a protein which binds transferin, a protein which binds lactoferin, and an opacity protein

said DNA being within an islet involved in the polonization of the nasopharynx or invasion of the submucousal space or systemic dissemination of Nm.

2. A composition comprising the DNA or complement of claim **1** and a carrier.

3. An isolated DNA which is specific to *Neisseria meningitidis* (Nm) and *Neisseria gonorrheae* (Ng), and hybridizes on a Southern blot to SEQ ID NO:95 and does not hybridize on a Southern blot to a DNA sequence of *Neisseria lactamica* (Nl) strain Nl8064, under the following hybridization conditions: 16 h at 65° C., with a solution comprising 0.5 M $NaPO_4$, pH 7.2, M EDTA-Na, 1% bovine serum albumin and 7% sodium dodecylsulphate, followed by at least two washes in a solution comprising 40 mM Na PO_4 pH7.2, 1 mM EDTA and 1% SDS, the final wash being conducted at 65° C. for 5 minutes, or the complement of said isolated DNA which is specific to *Neisseria meningitidis* (Nm) and *Neisseria gonorrheae* (Ng),

provided that said DNA or the complement of said isolated DNA is not pilC, or a gene involved in the biosynthesis of any one of the polysaccharide capsule, IgA proteases, pilin, a protein which binds transferrin, a protein which binds lactoferin, and an opacity protein.

4. A composition comprising the DNA or complement of claim **3** and a carrier.

5. A method of detecting *Neisseria meningitidis* (Nm) or *Neisseria gonorrheae* (Ng) in a sample from a patient said method comprising providing isolated sample DNA of said sample from the patient, contacting said sample DNA with the isolated DNA of claim **1**, said contacting being performed under conditions which allow hybridization of said sample DNA and said isolated DNA, and detecting any hybridization of said sample DNA and said isolated DNA, such that said hybridization of said sample DNA and said isolated DNA specifically indicates the presence of said Nm or Ng in said sample,

wherein said isolated DNA is specific to Nm and Ng and does not hybridize on a Southern blot to a DNA sequence of *Neisseria lactamica* (Nl) strain Nl8064 under the following hybridization conditions: 18 h at 65° C., with a solution comprising 0.5 M $NaPO_4$ pH 7.2, 0.001 M EDTA-Na, 1% bovine serum albumin and 7% sodium dodecylsulphate, followed by at least two washes in a solution comprising 40 mM Na PO_4 pH 7.2, 1 mM EDTA, and 1% SDS, the final wash being conducted at 65° C. for 5 minutes, and

wherein said isolated DNA specifically hybridizes to Nm DNA and Ng DNA in the presence of Nl DNA.

6. A method of detecting *Neisseria meningitidis* (Nm) or *Neisseria gonorrheae* (Ng) in a sample from a patient, said method comprising providing isolated sample DNA of said sample from the patient, contacting said sample DNA with the composition of claim **1** under conditions which a low hybridization of said sample DNA and DNA in said composition, and detecting any hybridization of said sample DNA and said DNA in said composition, such that said hybridization of said sample DNA and said DNA in said composition specifically indicates the presence of said Nm or Ng in said sample,

wherein said DNA in said composition is specific to Nm and Ng and does not hybridize on a Southern blot to a DNA sequence of *Neisseria lactamica* (Nl) strain Nl8064 under the following hybridization conditions: 16 h at 65° C., with a solution comprising 0.5 M $NaPO_4$ pH 7.2, 0.001 M EDTA-Na, 1% bovine serum albumin and 7% sodium dodecylsulphate, followed by at least two washes in a solution comprising 40 mM Na PO_4 pH 7.2, 1 mM EDTA, and 1% SDS, the final wash being conducted at 65° C. for 5 minutes, and

wherein said DNA is said composition specifically hybridizes to Nm DNA and Ng DNA in the presence of Nl DNA.

7. A method of detecting *Neisseria meningitidis* (Nm) of *Neisseria gonorrheae* (Ng) in a sample from a patient, said method comprising providing isolated sample DNA of said sample from the patient, contacting said sample DNA with the isolated DNA of claim **3**, said contacting being performed under conditions which allow hybridization of said sample DNA and said isolated DNA, and detecting any hybridization of said sample DNA and said isolated DNA, such that said hybridization of said sample DNA and said isolated DNA specifically indicates the presence of said Nm or Ng in said sample,

wherein said isolated DNA is specific to Mm and Ng and does not hybridize on a Southern blot to a DNA sequence of *Neisseria lactamica* (Nl) strain Nl8064 under the following hybridization conditions: 16 h at 65° C., with a solution comprising 0.5 M $NaPO_4$ pH 7.2, 0.001 M EDTA-Na, 1% bovine serum albumin and 7% sodium dodecylsulphate, followed by at least two washes in a solution comprising 40 mM Na PO_4pH 7.2, 1 mM EDTA, and 1% SDS, the final wash being conducted at 65° C. for 5 minutes, and

wherein said isolated DNA specifically hybridizes to Nm DNA and Ng DNA in the presence of Nl DNA.

8. A method of detecting *Neisseria meningitidis* (Nm) or *Neisseria gonorrheae* (Ng) in a sample from a patient, said method comprising providing isolated sample DNA of said sample from the patient, contacting said sample DNA with the composition of claim **4** under conditions which allow hybridization of said sample DNA and DNA in said composition, and detecting any hybridization of said sample DNA and said DNA in said composition, such that said hybridization of said sample DNA and said DNA in said composition specifically indicates the presence of said Nm or Ng in said sample,

wherein said DNA in said composition is specific to Nm and Ng and does not hybridize on a Southern blot to a DNA sequence of *Neisseria lactamica* (Nl) strain Nl8064 under the following hybridization conditions: 16 h at 65° C., with a solution comprising 0.5 M $NaPO_4$ pH 7.2, 0.001 M EDTA-Na, 1% bovine serum albumin and 7% sodium dodecylsulphate, followed by at least two washes in a solution comprising 40 mM Na PO_4 pH 7.2, 1 mM EDTA, and 1% SDS, the final wash being conducted at 65° C. for 5 minutes, and

wherein said DNA is said composition specifically hybridizes to Nm DNA and Ng DNA in the presence of Nl DNA.

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